

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 27, 2005, 20:02:49 ; Search time 115.869 Seconds
(without alignment)
1387.712 Million cell updates/sec

Title: US-10-040-647-6

Perfect score: 1728

Sequence: 1 MGARGALLALLARAGLRK.....PSWPLFFPLLWALPLGPV 314

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1723	99.7	314	1	TEST_HUMAN	Q9y6m0 homo sapien
2	1152	66.7	324	1	TEST_MOUSE	Q9jhj7 mus musculus
3	1152	66.7	336	2	Q80YD8	Q80ydh8 mus musculus
4	1128.5	65.3	328	2	Q80Z40	Q80z40 rattus norv
5	881	51.0	318	2	Q7RTY9	Q7rtv9 homo sapien
6	850	49.2	322	2	Q820S2	Q820s2 mus musculus
7	817	47.3	282	2	Q2D413	Q2d413 mus musculus
8	605	35.0	328	2	Q6BEA2	Q6bea2 rattus norv
9	597.5	34.6	321	2	Q6IE60	Q6ie60 rattus norv
10	596.5	34.5	321	1	TRYG_HUMAN	Q9nrr2 homo sapien
11	595.5	34.5	321	2	Q96R28	Q96rz8 homo sapien
12	586	33.9	719	2	Q6DJ90	Q6dj90 xenopus tro
13	585	33.9	328	2	Q8BJR6	Q8bjr6 mus musculus
14	579.5	33.5	343	1	PSS8_HUMAN	Q16651 homo sapien
15	575.5	33.3	389	2	Q9PVX7	Q9pvx7 xenopus lae
16	573	33.2	290	1	PR27_HUMAN	Q9bqr3 homo sapien
17	572.5	33.1	311	2	Q80XZ3	Q80xz3 rattus norv
18	570	33.0	330	2	Q6NVZ7	Q6nvz7 xenopus tro
19	567.5	32.8	339	2	Q93L44	Q93l44 mus musculus
20	567.5	32.8	342	1	PSS8_RAT	Q9es87 rattus norv
21	566.5	32.8	331	2	Q8RI66	Q8ri66 mus musculus
22	566	32.8	344	2	Q640F8	Q640f8 xenopus lae
23	565	32.7	321	2	Q6GNK3	Q6gnk3 xenopus lae
24	563.5	32.6	331	2	Q80X17	Q80x17 mus musculus
25	563.5	32.6	342	1	PSS8_MOUSE	Q9esdl mus musculus
26	561	32.5	317	2	Q9DGR3	Q9dgr3 xenopus lae
27	554.5	32.1	311	1	TRYG_MOUSE	Q9qul7 mus musculus
28	552	31.9	340	2	Q8BJV6	Q8bjv6 mus musculus
29	551	31.9	336	2	Q7RTV5	Q7rtv5 homo sapien
30	546.5	31.6	312	2	Q7M755	Q7m755 mus musculus
31	542	31.4	799	2	Q6PF94	Q6pf94 mus musculus

32	542	31.4	811	1	TMS6_MOUSE	Q9dbi0 mus musculus
33	541.5	31.3	309	2	Q6DHH4	Q6dhh4 brachydanio
34	539.5	31.2	307	2	Q7TMO0	Q7tmo0 mus musculus
35	539	31.2	273	1	TRYT_SHEEP	Q9xsm2 ovis aries
36	538.5	31.2	297	2	Q88781	Q88781 rattus ratt
37	536.5	31.0	317	1	BSS4_HUMAN	Q9gzn4 homo sapien
38	536.5	31.0	334	2	Q6UXE0	Q6uxe0 homo sapien
39	527.5	30.5	310	1	DISP_MOUSE	Q9gyz9 mus musculus
40	525	30.4	306	1	BSS4_MOUSE	Q9er10 mus musculus
41	523.5	30.3	270	1	TRYT_MERUN	P50342 meriones un
42	517.5	29.9	471	2	Q8CFE0	Q8cfe0 mus musculus
43	517	29.9	273	2	Q9XSM1	Q9xsm1 ovis aries
44	517	29.9	275	1	TRYT_PIG	Q9n2dl sus scrofa
45	513.5	29.7	638	1	KAL_MOUSE	P26262 mus musculus

ALIGNMENTS

RESULT 1
TEST_HUMAN
ID TEST_HUMAN STANDARD; PRT; 314 AA.
AC Q9y6m0; Q9NS34; Q9P2V6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Testisin precursor (EC 3.4.21.-) (Eosinophil serine protease 1) (ESP-1) (UNQ266/PRO303).
GN Name=PRSS21; Synonyms=ESPI, TESTI;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN RATTUS NORVIGICUS
SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Eosinophil;
RX MEDLINE=99045401; PubMed=9826525; DOI=10.1006/bbrc.1998.9645;
RA Inoue M., Kanbe N., Kurosawa M., Kido H.;
RT "Cloning and tissue distribution of a novel serine protease esp-1 from human eosinophils";
RL Biochem. Biophys. Res. Commun. 252:307-312(1998).
[2]
RN RATTUS NORVIGICUS
SEQUENCE FROM N.A. (ISOFORM 3).
RX MEDLINE=20068805; PubMed=10600542; DOI=10.1006/bbrc.1999.1870;
RA Inoue M., Isobe M., Itoyama T., Kido H.;
RT "Structural analysis of esp-1 gene (PRSS 21).";
RL Biochem. Biophys. Res. Commun. 266:564-568(1999).
[3]
RN RATTUS NORVIGICUS
SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Cervical carcinoma;
RX MEDLINE=99323395; PubMed=10397266;
RA Hooper J.D., Nicol D.L., Dickinson J.L., Eyre H.J., Scarman A.L., Normyle J.F., Stuttgen M.A., Douglas M.L., Loveland K.A., Sutherland G.R., Antalis T.M.;
RT "Testisin, a new human serine proteinase expressed by premetastatic testicular germ cells and lost in testicular germ cell tumors";
RL Cancer Res. 59:3199-3205(1999).
[4]
RN RATTUS NORVIGICUS
SEQUENCE FROM N.A.
RX MEDLINE=11004480; PubMed=11004480; DOI=10.1016/S0167-4781(00)00071-3;
RA Hooper J.D., Bowen N., Marshall H., Cullen L.M., Sood R., Daniels R., Stuttgen M.A., Normyle J.F., Higgs D.R., Kastner D.L., Ogbourne S.M., Pera M.F., Jazwinska E.C., Antalis T.M.;
RT "Localization, expression and genomic structure of the gene encoding the human serine protease testisin";
RL Biochim. Biophys. Acta 1492:63-71(2000).
[5]
RN RATTUS NORVIGICUS
SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P., Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heidens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,

Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojohori T.,
 Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 Blake J.A., Bradt D., Brusic V., Chochia C., Corbani L.E., Cousins S.,
 Dalla E., Dragani T.A., Fletcher C.P., Forrest A., Frazer K.S.,
 Gaasterland T., Gariboldi M., Giesi C., Godzik A., Gough J.,
 Grimmond S., Guetincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 Negashima T., Nunata K., Okido T., Pavan W.J., Perte G., Pesole G.,
 Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 Verardo R., Wagner L., Walstedt C., Wang Y., Watanabe Y., Wells C.,
 Wilming L.G., Wynshaw-Boris A., Yangisawa M., Yang L., Yang L.,
 Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 Birney E., Hayaishizaki Y.;
 "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs";
 Nature 420:563-573(2002).
 CC -1- FUNCTION: Could regulate proteolytic events associated with
 testicular germ cell maturation.
 CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
 (potential).
 CC -1- TISSUE SPECIFICITY: Testis.
 CC -1- DEVELOPMENTAL STAGES: Expressed in post-meiotic testicular germ
 cells.
 CC -1- SIMILARITY: Belongs to the peptidase S1 family.
 CC -1- CAUTION: Ref.3 sequence differs from that shown due to a stop
 codon in position 315.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC
 CC EMBL; AF304012; AAK29360.1; -;
 CC EMBL; AY005145; AAG02255.1; -;
 CC EMBL; AF176209; AAF64407.2; -;
 CC EMBL; AF226710; AAF64428.2; -;
 CC EMBL; AK006271; -; NOT_ANNOTATED_CDS.
 CC HSPSP; P00734; 1GHW.
 CC MEROPS; S01.011; -;
 CC MGD; MGI:1916698; Prss21.
 CC GO; GO:0005624; C:membrane fraction; IDA.
 CC GO; GO:0004252; F:serine-type endopeptidase activity; IDA.
 CC InterPro; IPR009003; Pept_Ser_Cys.
 CC InterPro; IPR001254; Peptidase_S1.
 CC InterPro; IPR001314; Peptidase_S1A.
 CC Pfam; PF00089; Trypsin; 1.
 CC PRINTS; PR00722; CHYMOTRYPSIN.
 CC PROSITE; PS50240; TRYPSIN_DOM; 1.
 CC PROSITE; PS00134; TRYPSIN_HIS; 1.
 CC PROSITE; PS00135; TRYPSIN_SER; 1.
 CC Glycoprotein; GPI-anchor; Hydrolase; Lipoprotein; Serine protease;
 KW Signal; Zymogen.
 FT SIGNAL 1 21 Potential.
 FT PROPEP 22 54 Potential.
 FT CHAIN 55 298 Testisin.
 FT PROPEP 299 324 Removed in mature form (Potential).
 FT ACT_SITE 95 95 Charge relay system (Potential).

FT	ACT_SITE	147	147	Charge relay system (Potential).
FT	ACT_SITE	248	248	Charge relay system (Potential).
FT	DISULFID	46	167	Potential.
FT	DISULFID	80	96	Potential.
FT	DISULFID	181	254	Potential.
FT	DISULFID	214	233	Potential.
FT	DISULFID	244	272	Potential.
FT	LIPID	298	298	GPI-anchor amidated asparagine (Potential).
FT	CARBOHYD	170	170	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	177	177	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	210	210	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	283	283	N-linked (GlcNAc. . .) (Potential).
FT	CONFLICT	275	275	P -> H (in Ref. 3).
SQ	SEQUENCE	324 AA;	36175 MW;	56DCS9B84F3CDD4 CRC64;

Query Match 66.7%; Score 1152; DB 1; Length 324;
 Best Local Similarity 65.0%; Pred. No. 1.9e-94;
 Matches 212; Conservative 38; Mismatches 60; Indels 16; Gaps 4;

Qy	1	MGARGALLALL--LARAGL-----	-----RKPESQEAAPLSPGCGRRVITSRIVGGED	47
Db	1	MGARGKTLVLLVVVATAAALQSTYLQVDPKPELQEPDLLSGPCGHRTPSRIVGGDD	60	
Qy	48	AEIGRPWQGSRLWDSHVCVSLSHRWALTAACFETYSYDLSLSDPSGVMWVQGLTSM	107	
Db	61	AEIGRPWQGSRLWGNHLCGATLLNRWVLTAAHCFQ--KD-NDPFDWTVQFGLTSRP	117	
Qy	108	SFSLQAYTYRYFVSNLYLSPRYLGNSPYDIALVKLSAPVYTKHIQICLOASTFEFEN	167	
Db	118	SLNLQAYSRYQIEDIFLPSKSEYQPNDAIKLSPPYNNFIQICLLNSTYKFN	177	
Qy	168	RTDCWVTGWGVIKEDALPSHTLQEVQVAIINNMCNHLFLKYSFRKIDFGDMVCAGNA	227	
Db	178	RTDCWVTGWAIGEDSLSPNTLQEVQVAIINNMCNHYKKPDFRTNIGDMVCAGTP	237	
Qy	228	QGGKDCFCGSGGCLACNKGDLWYQGVSWGVCGRPNRPGVYTNISHPEWIKLMAQ	287	
Db	238	EGGKDCFCGSGGCLACDQDTVMYQGVSWGVCGRPNRPGVYTNISHYNNIQSTMIR	297	
Qy	288	SGMSQDPSPWLLFFPLLWALPLGP	313	
Db	298	NGLRPDPVPLLLFLTLAWASSLLRP	323	

RESULT 3
 Q80YD8 PRELIMINARY; PRT; 336 AA.
 ID Q80YD8
 AC Q80YD8
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Prss21 protein (Fragment).
 GN Name=Prss21;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

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RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalusz D.E., Scherch A., Schein J.E.,
RA Jones S.J., Maira M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903 (2002).
RN [2]
RN RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Strausberg R.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; BC049588; AAH49588.1; -.
DR HSSP; P00766; 1CHG.
DR MGD; MGI:191698; Prss1.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0005624; C:membrane fraction; IDA.
DR GO; GO:0004252; F:serine-type endopeptidase activity; IDA.
DR GO; GO:0007283; P:spermatogenesis; TAS.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
FT NON TER 1
SQ SEQUENCE 336 AA; 37361 MW; E5206FEDBE55C670 CRC64;

Query Match 66.7%; Score 1152; DB 2; Length 336;
Best Local Similarity 65.0%; Pred. No. 1.9e-94;
Matches 212; Conservative 38; Mismatches 60; Indels 16; Gaps 4;

QY 1 MGARGALLALL--LARAGL-----RKPESEAAPLSGCGRRVITSRIYGGD 47
DB 13 MGARGTLVLLVVVATANAALQSTYLOVDPEKPELQDPLLSGCGHRTIPSRIVG 72
QY 48 AELGRWPQGSRLWDHSHVCSLLSHRWALTAHCFETYSDLSDPGSMVQFGQLTSM 107
DB 73 AELGRWPQGSRLVGNHLCATLLNRRWLTAHCFQ--KD-NDPFDWTVQFGELTSR 129
QY 108 SFWSLQAYTRYFVSNLYLSPRYLGNSPYDIALVKLSAPVYTKHQICLOASTFE 167
DB 130 SLNWLQAYSNNRYQIEDIFLSPKYSQEQPNIDIALKLSPPVYNNFIQPICLLNSTYKFEN 189
QY 168 RTDCWVTGWGVIKDEALPSPHTLQEVQVAIINNSMCHLFLKYSPEKDFGDMVCAGNA 227
DB 190 RTDCWVTGWGAIKDEALPSPHTLQEVQVAIINNSMCHLFLKYSPEKDFGDMVCAGT 249
QY 228 QGGKDAFCGSGGLACNKGDLWYQIGVSWGCGRPNRPVYTNISHHFEWIKLMAQ 287
DB 250 EGGKDAFCGSGGLACDQVTWYQVGSWVGICGCRPNRPVYTNISHHYNWIRLT 309
QY 288 SGMSQDPSPWPLFFPLLLPILGP 313
DB 310 NGLLRDPDPVPLLLFLTLAWASSLLRP 335

RESULT 4
Q80240 ID Q80240 PRELIMINARY; PRT; 328 AA.
AC Q80240;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Esinophil serine protease-1.
GN Name=resp-1;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RN RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Testis;
RA Nakamura Y., Inoue M., Okumura Y., Shiota M., Nishikawa M., Arase S.,
RA Kido H.;
RT "cloning, expression analysis, and tissue distribution of esp-
RT 1/testisin, a membrane-type serine protease from the rat.";
RL J. Med. Invest. 50:78-86(2003).
CC -1- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; AB074516; BAC57949.1; -.
DR HSSP; P00766; 1CHG.
DR MEROPS; S01.011; -.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 328 AA; 36631 MW; 7F6C0B204802B963 CRC64;

Query Match 65.3%; Score 1128.5; DB 2; Length 328;
Best Local Similarity 63.5%; Pred. No. 2.4e-92;
Matches 205; Conservative 40; Mismatches 59; Indels 19; Gaps 3;

QY 1 MGARGALLALLLARAGL-----RKPESEAAPLSGCGRRVITSRIYV 44
DB 1 MSARGTLVPLLVVVAVVEVTLQSTSSHVKVPDPEKPELQEANLLSGCGHRTIPSRIVG 60
QY 45 GEDAEELGRWPQGSRLWDHSHVCSLLSHRWALTAHCFETYSDLSDPGSMVQFGQLT 104
DB 61 GEEAEELGRWPQGSRLVGNHLCATLLNRRWLTAHCFQ--KD-NDPFDWTVQFGELT 117
QY 105 SFWSLQAYTRYFVSNLYLSPRYLGNSPYDIALVKLSAPVYTKHQICLOASTFE 164
DB 118 SRPSLWNLQAYSNNRYQIEDIFLSPKYTEQFPDIALKLSPPVYNNFIQPICLLNSTYK 177
QY 165 FENRTDCWVTGWGVIKDEALPSPHTLQEVQVAIINNSMCHLFLKYSPEKDFGDMVCA 224
DB 178 FANRTDCWVTGWGAIKDEALPSPHTLQEVQVAIINNSMCHLFLKYSPEKDFGDMVCA 237
QY 225 GNAQGGKDAFCGSGGLACNKGDLWYQIGVSWGCGRPNRPVYTNISHHFEWIKL 284
DB 238 GSPEGKDAFCGSGGLACDQVTWYQVGSWVGICGCRPNRPVYTNISHHYNWIRLT 297
QY 285 MAQSGMSQDPSPWPLFFPLLLWA 307
DB 298 MIRNGMLRDPDPVPLLLFLTLAWA 320

RESULT 5
Q7RTY9 ID Q7RTY9 PRELIMINARY; PRT; 318 AA.
AC Q7RTY9;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Testis serine protease 1 precursor.
GN Name=TESSP1;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2272134; PubMed=12838346;
RA Puentes X.S., Sanchez L.M., Overall C.M., Lopez-Otin C.;
RT "Human and mouse proteases: a comparative genomic approach.";
RL Nat. Rev. Genet. 4:544-558(2003).
CC -1- SIMILARITY: Belongs to peptidase family S1.
CC -1- MISCELLANEOUS: The sequence shown here is derived from an
CC ENBL/GenBank/DBJ third party annotation (TPA) entry.
DR EMBL; BN000124; CAD675.1; -.
DR HSP; P08709; 1FAK.
DR MEROPS; S01.327; -.
DR GO; GO:004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolyase; Protease; Serine protease; Signal.
FT SIGNAL 1 20
FT CHAIN 21 318 testis serine protease 1.
SQ SEQUENCE 318 AA; 35078 MW; D792213630CF15C3 CRC64;

Query Match 51.0%; Score 881; DB 2; Length 318;
Best Local Similarity 53.7%; Pred. No. 2.9e-70;
Matches 173; Conservative 45; Mismatches 84; Indels 20; Gaps 5;

QY 1 MGARGALLALLARAGLRKPESQEAAPLSCP-----CGRRVITSRIVGGE 46
DB 1 MGARGALLALLARAGLRKPESQEAAPLSCP-----CGRRVITSRIVGGE 46
QY 47 DAELGRWPQGSRLWDSHVGVSLLSHRWALTAACFCFETYSIDLSPSGMVMVQGLTSM 106
DB 60 ESARGRWPQASLRLLRRHRCGSLSSRRVWLSAHCFOKH---YPSSEWTVQLGELTSR 116
QY 107 PSFWSLQAYTRYFVSNLYLSPRYLGNPDYIALVKLSAPVYTKHIQICLQASTFEFE 166
DB 117 PTPWNLRAYSRYKVDIIVNPDALGVLRNDIALRLASSVYNYAIQICIESSTFNFV 176
QY 167 NRDCWVTGWGVIK-EDEALPSPHTLOEVQVVAIINNSMCHLFLKYSFRKDIIFGDMVCAG 225
DB 177 HRPCWVTGWGLISFGSTPLPPPPHREAOQTILNTRCNLYLFEQPSRSRWDSMFCAQ 236
QY 226 NAQGGKDACFGDSGGLACNKGDLWYQIGVSVGWGCGRPNRPGVYTNISHHFEWIKLM 285
DB 237 AEDGSVTCXGDSGGLVCDXGDLWYQIGVSVGWGCGRPNRPGVYTNISHHFEWIRVM 296
QY 286 AQSGMSQDPSPWPLFFPPLLWA 307
DB 297 SHS-TPRPNSQLLLALLWA 317

RESULT 6
Q920S2 ID Q920S2 PRELIMINARY; PRT; 322 AA.
AC Q920S2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Testis serine protease-1.
GN Name=4931440B09Rik; Synonyms=tessp-1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCB1_TaxID=10090;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

RP SEQUENCE FROM N.A.
RA Matsui H., Takano N., Takahashi T.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; AB049453; BAB68561.1; -.
DR HSP; P00766; 1CHG.
DR MEROPS; S01.417; -.
DR MGD; MGI:1918253; 4931440B09Rik.
DR GO; GO:0005615; C:extracellular space; TAS.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TYPD_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolyase; Protease; Serine protease.
SQ SEQUENCE 322 AA; 36218 MW; ED55F9A199A3E491 CRC64;

Query Match 49.2%; Score 850; DB 2; Length 322;
Best Local Similarity 52.8%; Pred. No. 1.7e-67;
Matches 172; Conservative 43; Mismatches 93; Indels 18; Gaps 6;

QY 1 MGARGALLALLARAGLRKPESQEAAP-----LSGPCRRVIT-SRIVGGEA 48
DB 1 MGQGPVLLLLLLC-VMLGKPGSRRESQAADLKSTDKLLSMPCGRNDTSRIVGGIES 59
QY 49 ELGRWPQGSRLWDSHVGVSLLSHRWALTAACFCFETYSIDLSPSGMVMVQGLTSMPS 108
DB 60 MQGRWPQASLRLLKXSHRCGSLSSRRVWLTAAHCFPKY--LDPEKWTVQLGQLTSKPS 116
QY 109 FWSLQAYTRYFVSNLYLSPRYLGNPDYIALVKLSAPVYTKHIQICLQASTFEFENR 168
DB 117 YMRKAYSGRYRYKDIIVNSEDKLS-HDLALLRLASSVYTNKDIQPCVQSPSTFSQH 175
QY 169 TDCWVTGWGVIKED-BALPSPHTLOEVQVVAIINNSMCHLFLKYSFRKDIIFGDMVCAGNA 227
DB 176 PRCWVTGWGVIQDLPLPPPHLREVOVQSVILNNSRCQELFEIFSLHLITKDVFCAG 235
QY 228 QGGKDACFGDSGGLACNKGDLWYQIGVSVGWGCGRPNRPGVYTNISHHFEWIKLMAQ 287
DB 236 DGSADTCSGDSGGLVCMMDGLWYQIGVSVGWGCGRPNLPGIYTNVSHYNNIETWML 295
QY 288 SGMSQDPSPWPLFFPPLLWALPLIGP 313
DB 296 NGAVRRDLALPLLSITLLOAPWLLRP 321

RESULT 7
Q9D4I3 ID Q9D4I3 PRELIMINARY; PRT; 282 AA.
AC Q9D4I3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus adult male testis cDNA, RIKEN full-length enriched
DE library, clone:4931440B09 product:TESTIS SERINE PROTEASE-1
DE homolog.
GN Name=4931440B09Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCB1_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
```



```
Db 170 SEQDLNPNRILOKLAFLIDTPKCNLLYSKDAEADIQLTKTIKDDMLCAGFAEGKDKACK 229
Qy 236 GDSGGPLACNDKGLWYQIGVSVGWGCGRRNRPQGVYTNISHHFWIQKLM-----AQ 287
Db 230 GDSGGPLVCLVDQSWQAGVISWEGCARRNRPQGVYTNISHHFWIQKLM-----AQ 287
Qy 288 SGMSQDPD-SW-PL 299
Db 290 SQQQORDPRGWQPL 303

RESULT 9
ID Q6IE60 PRELIMINARY; PRT; 321 AA.
AC Q6IE60;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Marapsin precursor.
GN Name=mpn;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX PubMed=15060002; DOI=10.1101/gr.1946304;
RA Puente X.S., Lopez-Otin C.;
RT "A genomic analysis of rat proteases and protease inhibitors.";
RL Genome Res. 14:609-622(2004).
CC -1- SIMILARITY: Belongs to peptidase family S1.
CC -1- MISCELLANEOUS: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ third party annotation (TPA) entry.
DR EMBL; BN000333; CAB48388.1; -
DR HSSP; P00734; 1BX.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001314; Peptidase_SIA.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF00089; Trypsin; 1.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Hydrolase; Protease; Serine protease; Signal.
FT SIGNAL 1 26 Potential.
FT CHAIN 27 321 marapsin.
SQ SEQUENCE 321 AA; 35053 MW; A87735DF7A52F9E1 CRC64;

Query Match 34.6%; Score 597.5; DB 2; Length 321;
Best Local Similarity 43.3%; Pred. No. 6.1e-45;
Matches 136; Conservative 38; Mismatches 99; Indels 45; Gaps 10;

Qy 6 ALLIALLARAGLRKPESQEAAPLSGPGRRVITSRIVGGDEALGRWPWGSLRLWDH 65
Db 8 ALLLLPLLRSLG-----PACGHRPMFRNRMVGGDALEGEWPFQVSIORGAH 55
Qy 66 VCGVSLLSHRWALTAACHFETYSDLSDPSGWNVPQGLTSMPSFWSLQ-----AYYTRYF 120
Db 56 FCGSLIAPTWWLIRAHCFST-----SDISIYQVILGAL-----KLOQPGFHALYVP-- 102
Qy 121 VSNIVLSPRYLZ-NSPYDIALVKLSAPVYTKHQIPICLQASTFEFENRTDCWVTGMGYI 179
Db 103 VKRVKSHPEYQGMASADVALVELQVPVTFKYILPCLPDPSPVVFVKGMCNWCWVGWSP 162
Qy 180 KEDEALPSFHTLOEVQVAIINSMCNHLFLKYSFR-----KILFGDMVCAAGQGGKACF 235
Db 163 SEQDLNPNRILOKLAFLIDTPKCNLLYSKDAEADIQLTKTIKDDMLCAGFAEGKDKACK 222
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Qy 236 GDSGGPLACNDKGLWYQIGVSVGWGCGRRNRPQGVYTNISHHFWIQKLM-----AQ 287
Db 223 GDSGGPLVCLVDQSWQAGVISWEGCARRNRPQGVYTNISHHFWIQKLM-----AQ 282
Qy 288 SGMSQDPD-SW-PL 299
Db 283 SQQQORDPRGWQPL 296

RESULT 10
TRYG HUMAN STANDARD; PRT; 321 AA.
ID Q9NR2; Q9C015; Q9NRQ8; Q9UB2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Tryptase gamma precursor (EC 3.4.21.-) (Transmembrane tryptase).
GN Name=TPSG1; Synonyms=TWI;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (VARIANTS GAMMA-1 AND GAMMA-2).
RX MEDLINE=20302813; PubMed=10843716;
RA Caughey G.H., Raymond W.W., Blount J.L., Hau L.W., Pallaro M.,
RA Wolters P.J., Verghese G.M.;
RT "Characterization of human gamma-tryptases, novel members of the
RT chromosome 16p mast cell tryptase and prostasin gene families.";
RL J. Immunol. 164:6566-6575(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99452974; PubMed=10521469; DOI=10.1074/jbc.274.43.30784;
RA Wong G.W., Tang Y., Feyfant E., Sali A., Li L., Li Y., Huang C.,
RA Friend D.S., Krilis S.A., Stevens R.L.;
RT "Identification of a new member of the tryptase family of mouse and
RT human mast cell proteases which possesses a novel COOH-terminal
RT hydrophobic extension.";
RL J. Biol. Chem. 274:30784-30793(1999).
RN [3]
RP SEQUENCE OF 220-321 FROM N.A.
RA Mittman S., Agnew W.S.;
RT "Organization and alternative splicing of CACNAH1.";
RC Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Membrane-anchored (Potential).
CC -1- TISSUE SPECIFICITY: Expressed in many tissues.
CC -1- POLYMORPHISM: There are two alleles, gamma-I and gamma-II which
CC differ by 5 residues.
CC -1- SIMILARITY: Belongs to the peptidase S1 family. Tryptase
CC subfamily.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC EMBL; AF191031; AAF76457.1; -
DR EMBL; AF195508; AAF76458.1; -
DR EMBL; AF175759; AAF03697.1; -
DR EMBL; AF175522; AAF03695.1; -
DR EMBL; AF223563; AAG48852.2; -
DR HSSP; P00760; 1EXX.
DR MEROPS; S01.028; -.
DR Genes; HGNC:14134; TPSG1.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001314; Peptidase_SIA.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
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[7]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Bladder;
RX MEDLINE=22433795; PubMed=12441343; DOI=10.1074/jbc.M209353200;
RA Bhagwandin V.J., Hau L.W., Mallen-St Clair J., Wolters P.J.,
CAughney G.H.;
RT "Structure and activity of human pancreas, a novel tryptic serine
RL peptidase expressed primarily by the pancreas.";
RL J. Biol. Chem. 5:3363-3371(2003).
[8]
RP SEQUENCE FROM N.A.
RC STRAIN=129/Sv;
RA Brathwaite M., Waeltz P., Schlössinger D., Nagaraja R.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; AK080281; BAC37864.1; -
DR EMBL; AF542056; AA027572.1; -
DR EMBL; AY162410; AA017162.1; -
DR HSPSP; P00734; 1UVS.
DR MEROPS; S01.074; -.
DR MGD; MG1:2450123; Mpn.
DR GO; GO:004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0006235; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001314; Peptidase S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF00089; Trypsin_1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYP_SPC; 1.
DR PROSITE; PS02040; TRYPIN_DOM; 1.
DR PROSITE; PS00134; TRYPIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 328 AA; 35789 MW; DC0B20F1AB3EB840 CRC64;

Query Match 33.9%; Score 585; DB 2; Length 328;
Best Local Similarity 44.2%; Pred. No. 8.1e-44;
Matches 129; Conservative 41; Mismatches 94; Indels 28; Gaps 8;

QY 6 ALLALLARAGLRKPSOEAPLPGCGRRVTSRVGGDAGLGNPWQGSRLRWDH 65
Db 8 ALLLLPPLLRSG-----TEGARTLRACGHPKMFNRMVGGENALGEGPWPQVSIQRNGIH 61
QY 66 VCGVSLLSHRWALTAACFETYSPLSDPSGWMVQFGOLTSNPSPWSLQ-----AYYTRYF 120
Db 62 FCGSLIAPTWTWLIARCF---SNTSDISIVQLLGLAL--KLQPGPHALYVP-- 109
QY 121 VSNITLSPRYLG-NSPYDIALVKLSAPVTVTKHIQICLQASTPEFENRTDCWVTGWYI 179
Db 110 VKQVKNPQYQGMASADVALVQLGPPVFTNYILPVCLPPSPVIFSGMNCWVTGWSP 169
QY 180 KEDALSPHTLOEVOVAIINNSCNHLF---LKYSPR-KDIFGDMVCAGNAQGGKDACF 235
Db 170 SEQDRLENPRVLQKLAVPIIDTPKCNLLYNKNDVESFQLTKIDMLCAGFAEKKDACK 229
QY 236 GDSGGPLACNDGLWYQIGVVMGCGCRPNRPVYTNISHHFWIOKLMQAQ 287
Db 230 GDSGGPLVCLVDQSWQAGVISWEGGCARRNRPQVYIRVTSHHKWIHQIIP 281

RESULT 14
PSS8 HUMAN
ID PSS8 HUMAN STANDARD; PRT; 343 AA.
AC Q16651; OYUCA3;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Proctasin precursor (EC 3.4.21.-).
GN Name=PRSS8;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

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OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Prostate;
RX MEDLINE=95286644; PubMed=7768952;
RY J.X., Chao L., Chao J.;
RT "Molecular cloning, tissue-specific expression, and cellular
RL localization of human proctasin mRNA.";
RL J. Biol. Chem. 270:13483-13489(1995).
[2]
RN SEQUENCE FROM N.A.
RP TISSUE=Placenta;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Tashiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[3]
RN SEQUENCE OF 45-64.
RP TISSUE=Semen;
RC MEDLINE=94308140; PubMed=8034638;
RX Yu J.X., Chao L., Chao J.;
RT "Proctasin is a novel human serine proteinase from seminal fluid.
RT Purification, tissue distribution, and localization in prostate
RT gland.";
RT J. Biol. Chem. 269:18943-18948(1994).
CC -!- FUNCTION: Possesses a trypsin-like cleavage specificity.
CC -!- SUBUNIT: Heterodimer of two chains, light and heavy, held by a
CC disulfide bond.
CC -!- SUBCELLULAR LOCATION: Membrane-bound. Secreted after cleavage of
CC its C-terminus.
CC -!- TISSUE SPECIFICITY: Found in prostate, liver, salivary gland,
CC kidney, lung, pancreas, colon, bronchus and renal proximal tubular
CC cells. In the prostate gland it may be synthesized in epithelial
CC cells, secreted into the ducts, and excreted into the seminal
CC fluid.
CC -!- SIMILARITY: Belongs to the peptidase S1 family.
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or send an email to license@isb-sib.ch).
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EMBL; L41351; AAC41759.1; -
EMBL; U33446; AAB19071.1; -
EMBL; BC001462; AAH01462.1; -
PIR; A57014; A57014.
HSPSP; P00760; 1EZX.
MEROPS; S01.159; -.
Genew; HGNC:9491; PRSS8.
H-InvDB; HIX0012982; -.
MIM; 600823; -.
GO; GO:0005615; C:extracellular space; TAS.
```

DR GO; GO:0005886; C:plasma membrane; TAS.
DR GO; GO:0008236; F:serine-type peptidase activity; TAS.
DR InterPro; IPR009003; Pept Ser Cys.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; Trypsin_1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Direct protein sequencing; Glycoprotein; Hydrolase; Serine protease;
KW Signal; transmembrane; Zymogen.
FT SIGNAL 1 29 Potential.
FT PROPEP 30 32 Activation peptide.
FT CHAIN 33 44 Proctasin light chain.
FT CHAIN 45 322 Proctasin heavy chain.
FT PROPEP 323 343
FT TRANSMEM 320 340 Potential.
FT DOMAIN 45 286 Serine protease.
FT DISULFID 37 154 Interchain (By similarity).
FT DISULFID 70 86 By similarity.
FT DISULFID 168 244 By similarity.
FT DISULFID 201 223 By similarity.
FT DISULFID 234 262 By similarity.
FT ACT_SITE 85 85 Charge relay system.
FT ACT_SITE 134 134 Charge relay system.
FT ACT_SITE 238 238 Charge relay system.
FT CARBOHYD 159 159 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 343 AA; 36431 MW; 98DD6447F5A8C1B2 CRC64;

Query Match 33.5%; Score 579.5; DB 1; Length 343;
Best Local Similarity 41.0%; Pred. No. 2.7e-43;
Matches 141; Conservative 45; Mismatches 101; Indels 57; Gaps 12;

QY 6 ALLALLARAGLRKPPSQEAPLSGCGRRVITSRVGGEDAEALGRWPNQGSRLRLWDH 65
DB 16 AILLYLGLLRSG-TGAEGAE-----PCG-VAQARITGGSSAVAGQMPQVSIYEGVH 68
QY 66 VCGVSLLSHWALTAACHFFETYSLDSPS-----GMMVQFG--QLTSMPSFWSLQAYYTR 118
DB 69 VCGSLVSEQWVLSANCF-----PSEHKAEYEVKLGAKQLDS-----YSEDAKVST 116
QY 119 YFVSNLYSPRYL-GNSPYDIALVKLSAPVYTKHIQICLOASTFEFENRTDCWVTG 177
DB 117 --LKDIIIPHSYLGEGSGDIALQLSRPITFSYIRIPICLPAANASFPNGLHCTVTG 174
QY 178 YKEDALPSHTLOFQVQVAIINSMCNHLP----LKYSFRKDFGDMVWCAGNAGGKDAC 234
DB 175 HVAPSVSLTPKPIQLQLEVLISRETNCNLYNIDAKPEEPHFQEDMVCAGYVEGGKDAC 234
QY 235 FGDSGGPLACNKGDLWYQIGVWSGVCGRRNRPVGTNISHHFEWIK-----KLMA 286
DB 235 QGDSGGPLSCPVEGLWYLTGLVSGDAGCARNRPGVYTLASSYASWISQSKTELQPRVP 294
QY 287 QSGMSQPDPSW-----PLIFPPLLWALPLLGP 313
DB 295 QTQESQPSNLCGSHLAFSSAPAQGLLRPIFLPLGLALGLLSP 338

RESULT 15

Q9PVX7 PRELIMINARY; PRT; 309 AA.
AC Q9PVX7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Epidermis specific serine protease.
OS Name=Xepsin;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
OC Xenopodinae; Xenopus.

OX NCBI_TaxID=8355;
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RP SEQUENCE FROM N.A.
RA Yamada K.;
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to peptidase family S1.
DR EMBL; A018694; BAA84941.1; -;
DR HSSP; P00760; 1EZX.
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DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR009003; Pept Ser Cys.
DR Pfam; PF00089; Trypsin_1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
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DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
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Best Local Similarity 39.9%; Pred. No. 6.9e-43;
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QY 140 LVKLSAPVYTKHIQICLOASTFEFENRTDCWVTGWTGWIKEDEALPSHTLOFQVQVAI 199
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DB 177 DSSVCGTMYESSIGYITDFSFIOE---DMVCAGYKEGRIDACQDSGGPLVCNNVNWMLQ 233
QY 253 IGVVSGVCGRRNRPVGTNISHHFEWIKMAQSGMSQPDPSWPLLPFLLWALPLLGP 312
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Search completed: February 27, 2005, 20:18:32
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LOCUS
DEFINITION
ACCESSION

VERSION	BD173076.1	GI:28414385	
KEYWORDS	JP 2002238587-A/211.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 1100)		
AUTHORS	Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and Yuan,J.		
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same		
JOURNAL	Patent: JP 2002238587-A 211 27-AUG-2002;		
COMMENT	GENENTECH INC		
	OS Homo sapiens (human)		
	PN JP 2002238587-A/211		
	PD 27-AUG-2002		
	PF 18-DEC-2001 JP 2001385248		
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	24-NOV-1997 US 60/066453,25-NOV-1997 US 60/066840 PI		
	WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI		
	UTAN ZHENG,		
	PI JEAN YUAN		
	PC C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC		
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	PC		
	C12P21/02,C12P21/08/(C12P21/02,C12R1:91),(C12P21/02,C12R1:19), PC		
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Gaps 0			
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Qy	121	ACGGGT	CAT	CA	CGT	CGCGCA	TCGTGGGT	GGAGAGGA	CGCCGAA	CTCGGGCG	TTTGGCCGTG	180
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Qy	181	GCAGGG	GAGC	CTCG	CGCTGT	GGGAT	CCCA	CGTATCGG	AGTAGAGC	CTGCTC	CAGCCACCG	240
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Qy	241	CTGGGCA	CTCA	CGCGCG	CGCA	CTGCTTTG	GAACCTATAGT	AGACTT	AGTATGAT	ATCCCTC	CGCG	300
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Qy	361	CTACACCG	TTACTT	CGTATCG	GAATATCTAT	CTGAGCCCTCG	TACTCTG	GGGAATTC	CACC			420
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Qy	421	CTATGCA	TTGCC	TTGGTGA	AGCTGTCTG	CACTGTCA	CCCTAC	CTAATAA	CACATCC	AGCC		480
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Qy	541	CTGGGGT	ATAC	CA	AAGAGAT	GAGGCAC	TGCCCAT	CTCCCCA	CACCTC	CAGGAG	TTTCA	600
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Qy	661	GGACAT	CTTTTGG	AGACAT	GTGTTGT	GCTGCA	ATGCCCA	AGGGG	GAAGGAT	GCCTG	CTT	720
Db	664	GGACAT	CTTTTGG	AGACAT	GTGTTGT	GCTGCA	ATGCCCA	AGGGG	GAAGGAT	GCCTG	CTT	723
Qy	721	CGGTG	ACTC	AGTGG	AGACCTTGG	CTGTAA	CAAGGAT	GGAGTGT	GTGAT	CAGATTG	GAGT	780
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Qy	781	CGTGAG	CTGGG	AGTGG	GTGTGT	GGCCCA	ATCGGCC	CGTGTCTAC	ACCAATAT	FCAG		840
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Qy	901	CTCTG	GGCGCT	ACTCT	TTTTTCC	CTTCTT	CTGTGG	GTCTCC	CACTCT	CTGGG	CGCGTGTG	960
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Qy	961	AGCTACT	CTAG	CCCA	TG	CGACCTGG	GGCCACTG	CCAAAGT	CAGGCC	CTGTCT	CTCTG	1020
Db	964	AGCTACT	CTAG	CCCA	TG	CGACCTGG	GGCCACTG	CCAAAGT	CAGGCC	CTGTCT	CTCTG	1023
Qy	1021	TCCTG	TTTGGT	ATAA	CACAT	TC	AGTGTG	ATGCTT	GTGAGGG	CATTTTT	CAAAAAAAA	1080
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BD173395

LOCUS

BD173395

1100 bp

DNA

linear

PAT 18-FEB-2003

RESULT 5
BD173395
LOCUS

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Qy 301 GTGATGTCAGTTGCGGAGCTGACTTCCATGCCATCTCTGAGCGCTGCGAGGCGCTA 360
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Qy 481 CATCTGCTCCAGCGCTCCCATTTGAGTTGAGAAACCGACACACTGCTGGGGTACTGG 540
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Qy 841 CCACCATTTGAGTGGATCCAGAGCTGATGGCCAGAGTGGCATGTCCAGCCAGACCC 900
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BD175429
LOCUS
DEFINITION
Secretory and transmembrane polypeptide and nucleic acid encoding the same.
ACCESSION
BD175429
VERSION
BD175429.1 GI:29121127
KEYWORDS
JP 2002253280-A/211.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1100)
AUTHORS
Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and Yuan,J.
TITLE
Secretory and transmembrane polypeptide and nucleic acid encoding the same
JOURNAL
GENENTECH INC
COMMENT
Patent: JP 2002253280-A 211 10-SEP-2002;
PN JP 2002253280-A/211
PD 10-SEP-2002
PR 18-DEC-2001 JP 2001385319
PR 17-SEP-1997 US 60/059115, 17-SEP-1997 US 60/059184 PR
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WILLIAM I WOOD, AUSTIN L GURNEY, AUDREY GODDARD, DIANE PENNICA, PI
JIAN ZHENG,
PI JEAN YUAN
PC C12N15/09, A61K45/00, A61P1/00, A61P13/12, A61P17/00, A61P17/06, PC
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Best Local Similarity 99.6%; Pred. No. 1.5e-264;

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DEFINITION	Sequence 256 from patent US 6664376.		
ACCESSION	AR439172		
VERSION	AR439172.1	GI:42665021	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 1100)		
AUTHORS	Ashkenazi, A., Botstein, D., Desnoyers, L., Eaton, D.L., Ferrara, N., Filvaroff, E., Fong, S., Gao, W.-Q., Gerber, H., Gerritsen, M.E., Goddard, A., Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Hillan, K.J., Kljavin, I.J., Mather, J.P., Pan, J., Paoni, N.F., Roy, M.A., Stewart, T.A., Tumas, D., Williams, P.M. and Wood, W.I.		
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same		
JOURNAL	Patent: US 6664376-A 256 16-DEC-2003;		
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Qy	1	CGCGGAGAGGAGGCCATGGCGCGCGCGCGCGCTGCTGCTGGCGGTGCTGCTGGCTCG	60
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Qy	661	GGACATCTTTGGAGACATGTTTGTCTGGCAATGCCAAGCGGGAAGATGCTGCTTT	720
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Qy	1081	AAAAAAAAAAAAAAAA 1097	
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AUTHORS	Desnoyers, L., Goddard, A., Godowski, P.J., Gurney, A.L. and Wood, W.I.									
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same									
JOURNAL	Patent: US 6767995-A 256 27-JUL-2004;									
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The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment
Genome Res. 13 (10), 2265-2270 (2003)

JOURNAL

PUBMED

REFERENCE

2 (bases 1 to 1100)

AUTHORS

Clark, H.F.

Direct Submission

Submitted (01-AUG-2003)

Department of Bioinformatics, Genentech,

Inc., 1 DNA Way, South San Francisco, CA 94080, USA

Location/Qualifiers

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QY 355 CTACACCGCTTACTTGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGGAAATTCACC 414
Db |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 421 CTATGACATTCCTTGTGAGCTGTCTGACCTGTCTACCTTACCTAAACACATCCAGCC 480
Db |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 415 CTATGACATTCCTTGTGAGCTGTCTGACCTGTCTACCTTACCTTAAACACATCCAGCC 474
Db |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 481 CATCTGTCTCCAGCCCTCCATTTGAGTTTGAACCGGACAGACTGTCTGGGTGACTGG 540
Db |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 475 CATCTGTCTCCAGCCCTCCATTTGAGTTTGAACCGGACAGACTGTCTGGGTGACTGG 534
Db |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 541 CTGGGGGTACATCAAGAGGATGAGGACCTGCCATCTCCACACACCTCCAGGAGTTCA 600
Db |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 535 CTGGGGGTACATCAAGAGGATGAGGACCTGCCATCTCCACACACCTCCAGGAGTTCA 594
Db |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 601 GGTCCCATCAATAAACAACTCTATGTGCAACCACTCTTCTCAAGTACAGTTTCCGCAA 660
Db |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 595 GGTCCCATCAATAAACAACTCTATGTGCAACCACTCTTCTCAAGTACAGTTTCCGCAA 654
Db |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 661 GGACATCTTTGGAGACATGTTGTGTGGCAATGCCCAAGCGGGGAGGATGCTGCTT 720
Db |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 655 GGACATCTTTGGAGACATGTTGTGTGGCAATGCCCAAGCGGGGAGGATGCTGCTT 714
Db |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 721 CGGTGACTCAGGTGGACCTTGGCTGTAAACAGGATGGAAGTGTGTATCAGATTGGAGT 780
Db |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 715 CGGTGACTCAGGTGGACCTTGGCTGTAAACAGGATGGAAGTGTGTATCAGATTGGAGT 774
Db |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 781 CGTGAGCTGGGGAGTGGCTGTGTGGCCCAATCGGCCCGGTGTCTACACCAATATCAG 840
Db |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 775 CGTGAGCTGGGGAGTGGCTGTGTGGCCCAATCGGCCCGGTGTCTACACCAATATCAG 834
Db |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 841 CCACCACTTTGAGTGGATCCAGAGCTGATGGCCAGAGTGGCATGTCCAGCCAGACCC 900
Db |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 835 CCACCACTTTGAGTGGATCCAGAGCTGATGGCCAGAGTGGCATGTCCAGCCAGACCC 894
Db |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 901 CTCTGGCGCTTACTCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 960
Db |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 895 CTCTGGCGCTTACTCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 954
Db |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 961 AGCCTACTGAGCCCATGAGCTGGGGCCATGCGCAAGTCAGGCCCTGGTTCTTCTG 1020
Db |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 955 AGCCTACTGAGCCCATGAGCTGGGGCCATGCGCAAGTCAGGCCCTGGTTCTTCTG 1014
Db |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1021 TCTTGTGTTGTTAATAAACACATTCAGTTGATGCTTGCAGGGCAATTTTCAAAAAAAA 1080
Db |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1015 TCTTGTGTTGTTAATAAACACATTCAGTTGATGCTTGCAGGGCAATTTTCAAAAAAAA 1074
Db |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1081 AAAAAAAAAAAAAAAAAAAAA 1100
Db |||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1075 AAAAAAAAAAAAAAAAAAAAA 1094
Db |||||||||||||||||||||||||||||||||||||||||||||||||||
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 27, 2005, 20:11:50, Search time 25.5815 Seconds
(without alignments)
1181.014 Million cell updates/sec

Title: US-10-040-647-6
Perfect score: 1728
Sequence: 1 MGARGALLALLARAGLRK.....PSWPLLPFLWALPLLPV 314

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR.79:.*
1: Pir1.*
2: Pir2.*
3: Pir3.*
4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	579.5	33.5	343	1 A57014	proctasin (EC 3.4.21.1)
2	523.5	30.3	270	2 S56160	mast cell tryptase
3	513.5	29.7	638	1 KQMSPL	plasma kallikrein
4	513	29.7	275	2 C35863	tryptase (EC 3.4.21.1)
5	511	29.6	276	2 A38654	mast cell proteinase
6	510	29.5	275	2 A35863	tryptase (EC 3.4.21.1)
7	510	29.5	638	1 KQRTPL	plasma kallikrein
8	509	29.5	273	2 A47246	tryptase (EC 3.4.21.1)
9	509	29.5	275	2 B35863	tryptase (EC 3.4.21.1)
10	509	29.5	275	2 A32410	tryptase (EC 3.4.21.1)
11	507	29.3	638	1 KQHP	plasma kallikrein
12	499	28.9	274	2 JC4171	tryptase (EC 3.4.21.1)
13	498.5	28.8	274	2 A45754	tryptase (EC 3.4.21.1)
14	478.5	27.7	625	1 KFHU1	coagulation factor
15	476.5	27.6	417	1 S00845	hepsin (EC 3.4.21.1)
16	474.5	27.5	366	2 JE0105	testicular serine
17	457.5	26.5	415	1 A34170	acrosin (EC 3.4.21.1)
18	457.5	26.5	436	2 JC4171	acrosin (EC 3.4.21.1)
19	454.5	26.3	810	1 PLHU	plasmin (EC 3.4.21.1)
20	454	26.3	855	2 JC7731	membrane-bound arg
21	453	26.2	455	2 A61545	plasmin (EC 3.4.21.1)
22	451.5	26.1	237	2 S88702	tryptase (EC 3.4.21.1)
23	446	25.8	416	1 S33777	hepsin (EC 3.4.21.1)
24	443.5	25.7	4548	1 S00657	apoptein(a) (EC
25	443	25.6	1113	2 JE0315	low-density lipopr
26	441	25.5	1035	1 A43090	enteropeptidase (E
27	439.5	25.4	421	2 S29599	acrosin (EC 3.4.21.1)
28	439	25.4	367	2 JE0104	testicular serine
29	438	25.3	1019	1 A56318	enteropeptidase (E

30 436.5 25.3 460 2 B61545 plasmin (EC 3.4.21.1)

31 435 25.2 786 1 A47547 serine proteinase

32 435 25.2 810 2 B30848 plasmin (EC 3.4.21.1)

33 434.5 25.1 418 2 A37344 acrosin (EC 3.4.21.1)

34 434.5 25.1 812 1 PLMS plasmin (EC 3.4.21.1)

35 433 25.1 790 1 PLPG plasmin (EC 3.4.21.1)

36 432 25.0 421 1 S11674 acrosin (EC 3.4.21.1)

37 432 25.0 812 1 FLBO plasmin (EC 3.4.21.1)

38 431.5 25.0 431 2 S47538 acrosin (EC 3.4.21.1)

39 428.5 24.8 437 2 S18407 acrosin (EC 3.4.21.1)

40 427.5 24.7 266 2 S54146 trypsin (EC 3.4.21.1)

41 427 24.7 810 2 I46260 plasmin (EC 3.4.21.1)

42 426 24.7 1420 2 A32869 apolipoprotein(a)

43 421 24.4 1524 2 T30337 polyprotein - Afri

44 416 24.1 761 2 JC5759 brain-specific ser

45 413 23.9 269 2 B32410 mastocytoma protei

ALIGNMENTS

proctasin (EC 3.4.21.1) precursor - human

C;Species: Homo sapiens (man)

C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004

C;Accession: A57014; A54866

R;Yu, J.X.; Chao, L.; Chao, J.

J. Biol. Chem. 270, 13483-13489, 1995

A;Title: Molecular cloning, tissue-specific expression, and cellular localization of hum

A;Reference number: A57014; MUID:95286644; PMID:7768952

A;Accession: A57014

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-343 <RES>

A;Cross-references: UNIPROT:Q16651; GB:L41351; NID:g862304; PIDN:AAC41759.1; PID:g862305

A;Experimental source: prostate

A;Note: parts of this sequence were determined by protein sequencing

R;Yu, J.X.; Chao, L.; Chao, J.

J. Biol. Chem. 269, 18843-18848, 1994

A;Title: Proctasin is a novel human serine proteinase from seminal fluid. Purification, t

A;Reference number: A54866; MUID:94308140; PMID:8034638

A;Accession: A54866

A;Molecule type: protein

A;Residues: 45-64 <YUA>

C;Genetics:

A;Gene: GDB:PRSS8

A;Cross-references: GDB:676446; OMIM:600823

A;Map position: 16p11.2-16p11.2

C;Superfamily: trypsin; trypsin homology

C;Keywords: glycoprotein; hydrolase; serine proteinase; transmembrane protein

F;1-32/Domain: signal sequence #status predicted <SIG>

F;33-44, 45-343/Product: proctasin #status predicted <MAT>

F;33-44/Domain: proctasin light chain #status predicted <CHL>

F;45-343/Domain: proctasin heavy chain #status predicted <CHH>

F;45-281/Domain: trypsin homology <TRY>

F;323-341/Domain: transmembrane #status predicted <TM1>

F;37-154, 70-86, 168-244, 201-223, 234-262/Disulfide bonds: #status predicted

F;85, 134, 238/Active site: His, Asp, Ser #status predicted

F;159/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 33.5%; Score 579.5; DB 1; Length 343;

Best Local Similarity 41.0%; Pred. No. 2.8e-44;

Matches 141; Conservative 45; Mismatches 101; Indels 57; Gaps 12;

Qy 6 ALLIALLARAGLRKPSQEAAPLSGCGRRVTSRVGGEDALGWPQGSRLWDSh 65

Db 16 ALLYGLLRSG-TGAEAE-----PCG-VAQARITGGSSAVAGQWPQVSYIEGVH 68

Qy 66 VCGVSLSHRWALTAHCFPTYSDLSDPS-----GMMVQFG--OLTSMPSPFWSLQAVYTR 118

Db 69 VCGSLVSEQWVLSAHCF-----PSEHKEAYEVKLGAKHQLDS-----YSEDAKVST 116

F;32-268/Domain: trypsin homology <TRY>
F;75,122,225/Active site: His, Asp, Ser #status predicted

Query Match 29.6%; Score 511; DB 2; Length 276;
Best Local Similarity 39.3%; Pred. No. 3e-38;
Matches 106; Conservative 42; Mismatches 88; Indels 34; Gaps 9;

QY 32 PCGRVITTSRIVGGEDAEELRWPGQSLRL-----WDSHVCVGVSLLSHRWALTAAHCFETY 87
Db :|||:|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:
25 PANQRV---GIVGHEASESKWPQWSLRFKLNYM--IHFCGGLIHPQWLVTAAHCVGPH 80
QY 88 SLDSDPSGMVVQFGQLTSMPSFWLSQAYTRY-----FVSNLYLSPR-YLGNSPYDIALV 141
Db :|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:
81 --TKSPOLFVRQ-----LRBQLYYGDLISLNRIVVHPHYTAAEGGDVAALL 126
QY 142 KLSAPVTTYTHIQICLOASTFEENRTDCWVTGWGYIKEDALPSPHTLQSVQVAII NN 201
Db 127 ELEVPVNVSTHIPIISLPASETFFPGTSCWVTGNGIDINDEPLPPPPYLKQVKPVIVEN 186
QY 202 SMCNHLFLKYTSFRKDIF----GDMVCAGNAOGGKADCEGDSGGGPLACNKDGLWYQIGVVS 257
Db 187 SLCDRKVHTGLTYGTDDFPFIHDGMLCAGNTR--RDSCQDGGGPLCKYKGTLQAGVVS 244
QY 258 WGVCGCRPNRPBGVYTNISSHFFEWIKLMAQ 287
Db |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:
245 WGECAQPNRPGIYTRYTYLDWIHRYPVE 274

RESULT 6
A35863
C:Species: Homo sapiens (man)
C>Date: 12-Oct-1990 #sequence revision 12-Oct-1990 #text_change 09-Jul-2004
C:Accession: A35863; D35863; A60939; A39326
R:Vanderslice, P.; Ballinger, S.M.; Tam, E.K.; Goldstein, S.M.; Craik, C.S.; Caughey, G.
Proc. Natl. Acad. Sci. U.S.A. 87, 3811-3815, 1990
A>Title: Human mast cell tryptase: multiple cDNAs and genes reveal a multigene serine pr
A:Reference number: A35863; MUID:90251647; PMID:2187193
A:Accession: A35863
A:Molecule type: DNA
A:Residues: 1-275 <VAN>
A:Cross-references: UNIPROT.Q15661; GB:M33494; NID:g3927804; PIDN:AAC83172.1; PID:g33997;
A:Accession: D35863
A:Molecule type: mRNA
A:Residues: 1-275 <VA2>
A:Cross-references: GB:M33491
R:Butterfield, J.H.; Weller, D.A.; Hunt, L.W.; Wynn, S.R.; Roche, P.C.
J. Leukoc. Biol. 47, 409-419, 1990
A>Title: Purification of tryptase from a human mast cell line.
A:Reference number: A60939; MUID:90244210; PMID:2110591
A:Accession: A60939
A:Molecule type: protein
A:Residues: 31-38, 'P', 40-41, 'X', 43, 'T', 45-48, 'X', 50 <BUT>
A:Experimental source: mast cell
R:Notomi, H.; Seidah, N.G.; Marcinkiewicz, M.; Hamelin, J.; Johnson, D.A.; Chretien,
J. Biol. Chem. 262, 1363-1373, 1987
A>Title: Human pituitary tryptase: molecular forms, NH-2-terminal sequence, immunocytoche
A:Reference number: A39326; MUID:87109258; PMID:3543004
A:Accession: A39326
A:Molecule type: protein
A:Residues: 31-38 <CRO>
A:Experimental source: pituitary
C:Genetics:
A:Introns: 21/1; 78/2; 177/1; 221/3
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; serine proteinase; zymogen
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-30/Domain: activation peptide #status predicted <ACT>
F;31-275/Product: tryptase I #status experimental <MAT>
F;31-267/Domain: trypsin homology <TRY>
F;74,121,224/Active site: His, Asp, Ser #status predicted

Db 119 DIALKLTNPVNI SDYVHPVPLPASETPPSGTLCWVTGWNIDNGVNLPPFPPLKQV 178

Qy 197 AIINSMCNHLFLKYSPFRD-----IFGDMVCAGNAGQGGKDA 252

Db 179 PIENHLCDLKYHKLITGDNVHIVRDDMLCAGNE--GHDSCQDGGGGLVCKVEDTWLQ 236

Qy 253 IGUVSWGGCGRPNRPVGVYTNISHHFEWI 281

Db 237 AGVWSWGGCAQPNRPPIYTRVYYLDWI 265

RESULT 9

B35863

tryptase (EC 3.4.21.59) II precursor - human

N;Alternate names: tryptase beta

C;Species: Homo sapiens (man)

C;Date: 03-Feb-1994 #sequence revision 03-Feb-1994 #text_change 09-Jul-2004

C;Accession: B35863; A37193; I59473

R;Vanderlisse, P.; Ballinger, S.M.; Tam, E.K.; Goldstein, S.M.; Craik, C.S.; Caughey, G. Proc. Natl. Acad. Sci. U.S.A. 87, 3811-3815, 1990

A;Title: Human mast cell tryptase: multiple cDNAs and genes reveal a multigene serine protease

A;Reference number: A35863; MUID:90251647; PMID:2187193

A;Accession: B35863

A;Molecule type: mRNA

A;Residues: 1-275 <VAN>

A;Cross-references: UNIPROT:P20231; GB:M33492; NID:g339982; PIDN:AAA36779.1; PID:g339983

A;Note: Residues 2-275 are derived from mRNA; residue one was inferred from the genomic

R;Miller, J.S.; Moxley, G.; Schwartz, L.B. J. Clin. Invest. 86, 864-870, 1990

A;Title: Cloning and characterization of a second complementary DNA for human tryptase.

A;Reference number: A37193; MUID:90369005; PMID:2203827

A;Accession: A37193

A;Molecule type: mRNA

A;Residues: 1-275 <MIL>

A;Cross-references: GB:M37488; NID:g179583; PIDN:AAA51843.1; PID:g179584

R;Blom, T.; Hellman, L. 37, 203-208, 1993

Scand. J. Immunol.

A;Title: Characterization of a tryptase mRNA expressed in the human basophil cell line K562

A;Reference number: I59473; MUID:93166209; PMID:8434231

A;Accession: I59473

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-275 <RES>

A;Cross-references: GB:S5551; NID:g265666; PIDN:AAD13876.1; PID:g4261576

A;Experimental source: basophil cell line KU812

C;Genetics:

A;Gene: GDB:TPS1

A;Cross-references: GDB:125890; OMIM:191080

A;Map position: 16pter-16qter

C;Superfamily: trypsin; trypsin homology

C;Keywords: hydrolase; serine proteinase; zymogen

F;1-21/Domain: signal sequence #status predicted <SIG>

F;22-30/Domain: activation peptide #status predicted <ACT>

F;31-275/Product: tryptase I #status predicted <MAT>

F;31-267/Domain: trypsin homology <TRY>

F;74,121,224/Active site: His, Asp, Ser #status predicted

Query Match 29.5%; Score 509; DB 2; Length 275;

Best Local Similarity 39.9%; Pred. No. 4.6e-38;

Matches 115; Conservative 43; Mismatches 92; Indels 38; Gaps 11;

Qy 7 LLLAL--LLAPAGLRKPESQEAAPLSPGCGRRVITSRVGGEDAEALGRWPQGSRLRL--- 61

Db 5 LLLALPVLASRA-----YAAPAGQALQV---GIVGQEAAPRSKWPQVSLRVHGP 53

Qy 62 -WDSHVCVSLSHRWALTAAHCFTETSDLSDPGWMVQFQLTSMFWSLQAYTYRYP 120

Db 54 YW-NHFCGSGSLHPQWVLTAAHC--VGPDKVLAALRVQLRE-----QHLYYQDQL 101

Qy 121 --VSNIVLSRP-VLGNSPYDIALVKLSAPVYTKHIQICLQASTFEFENRTDCWVTG 177

Db 102 LPVSRIVHPQFYTAQIGADIALLEBEPVKVSHVHTVLPASSETFPFGMPCWVTG 161

Qy 178 YIKEDALPSPHTLOEVQVVAIINSMCNHLFLKYSPFRD-----IFGDMVCAGNAGQGGKDA 233

Db 162 DVNDERLPPFPFLKQVKVPMENHI CDAYHLGAYTGDDVRI VRDDMLCAGNTR--RDS 219

Qy 234 CFGDSGGPLACNKDGLWVQIGVWSWGGCGRPNRPVGVYTNISHHFEWI 281

Db 220 CQDSSGGLPVCKVNGTWLQAGVWSWGGCAQPNRPPIYTRVYYLDWI 267

RESULT 10

A32410

tryptase (EC 3.4.21.59) precursor - dog

C;Species: Canis lupus familiaris (dog)

C;Date: 12-Oct-1989 #sequence revision 12-Oct-1989 #text_change 09-Jul-2004

C;Accession: A32410

R;Vanderlisse, P.; Craik, C.S.; Nadel, J.A.; Caughey, G.H. Biochemistry 28, 4148-4155, 1989

A;Title: Molecular cloning of dog mast cell tryptase and a related protease: structural

A;Reference number: A32410; MUID:89352460; PMID:2504277

A;Molecule type: mRNA

A;Residues: 1-275 <VAN>

A;Cross-references: UNIPROT:P15944; GB:M24664; NID:g163982; PIDN:AAA30854.1; PID:g163983;

C;Superfamily: trypsin; trypsin homology

C;Keywords: hydrolase; serine proteinase; zymogen

F;1-21/Domain: signal sequence #status predicted <SIG>

F;22-30/Domain: activation peptide #status predicted <ACT>

F;31-275/Product: tryptase #status predicted <MAT>

F;31-267/Domain: trypsin homology <TRY>

F;74,121,224/Active site: His, Asp, Ser #status predicted

Query Match 29.5%; Score 509; DB 2; Length 275;

Best Local Similarity 40.6%; Pred. No. 4.6e-38;

Matches 116; Conservative 40; Mismatches 98; Indels 32; Gaps 11;

Qy 9 LALLAPAGLRKPESQEAAPLSPGCGRRVITSRVGGEDAEALGRWPQGSRLRL---WDS 64

Db 5 LVLALALGSLVPSV---PAPQALQV---GIVGQEAAPGSKWPQVSLRLKQYWR 56

Qy 65 HVCVSLSHRWALTAAHCFTETSDLSDPGWMVQFQLTSMPSFWSLQAYTYRYP--VS 122

Db 57 HICGSLIHPQWVLTAAHC--VGPNVVCPPIRVQLRE-----QHLYYQDHLPLVN 105

Qy 123 NYLSRP-VLGNSPYDIALVKLSAPVYTKHIQICLQASTFEFENRTDCWVTGWIKE 181

Db 106 RIVMHPNYYTPENGADIALLEDEPNVSAHVQVTLPPALQTEPTCTPCWVTGWDVHS 165

Qy 182 DEALPSPHTLOEVQVVAIINSMCN---HLFLKYSFR-KDIFGDMVCAGNAGQGGKDA 237

Db 166 GTPLPFPFLKQVKVPIVENSMDVQVHLGLSTGQGVRIVRREDMLCAGNSK--SDSCQGD 223

Qy 238 SGGPLACNKDGLWVQIGVWSWGGCGRPNRPVGVYTNISHHFEWIQK 283

Db 224 SGGPLVCRVGVWVLTAAHC--VGPNVVCPPIRVQLRE-----QHLYYQDHLPLVN 269

RESULT 11

KOHUP

Plasma kallikrein (EC 3.4.21.34) precursor - human

N;Alternate names: kininogenin; plasma prekallikrein

C;Species: Homo sapiens (man)

C;Date: 13-Aug-1986 #sequence revision 13-Aug-1986 #text_change 09-Jul-2004

C;Accession: A00921; A37939

R;Chung, D.W.; Fujikawa, K.; McMullen, B.A.; Davie, E.W. Biochemistry 25, 2410-2417, 1986

A;Title: Human plasma prekallikrein, a zymogen to a serine protease that contains four trypsin-like domains

A;Reference number: A00921; MUID:86243359; PMID:3521732

A;Accession: A00921

A;Molecule type: mRNA

A;Residues: 1-638 <CHU>

A;Cross-references: UNIPROT:P03952; GB:M13143; NID:g190262; PIDN:AAA60153.1; PID:g190263

R;McMullen, B.A.; Fujikawa, K.; Davie, E.W. Biochemistry 30, 2050-2056, 1991

Db 5 LLLALPVLASRAYAPAPVQALQAG-----IVGGQAPRSKWPQVSLRVVDRY 54
Qy 64 -SHVCGVSLSHRWALTAACHFETYSYDLSPSGMWVQFGLTSMPSFWSLQAYTRYF-- 120
Db 55 WMHFCGSLIHPQVLTAAHCLG--PDVKLATLRVNSG-----THLYYQDQLLP 102
Qy 121 VSNLYLSPR-YLGNSPVDIALVKSAPVYTKHTQICLOASTFEFENRTDCWVTGWYI 179
Db 103 VSRIMVHPQFYIITGADIALLELEFPVNISSRVHTVMLPPASSTFFPGMPCWVTGWGDV 162
Qy 180 KEDEALSPHTLOEQVQVAINNSMCHLFLKYSFKD-----IFGDMVCAAGNAQGGKACF 235
Db 163 DNDPLPPPLPKQVPIEMENHICDAKYHLGATGDDVLIIRDMLCAGNSQ--RDSCK 220
Qy 236 GDSGGPLACNKGQWYQIGVSVGWGCGRPNRPVGYTNISHHFEWI 281
Db 221 GDSGGPLVCKVNGTWLQAGVSVWDEGCAQPNRPGIYTRVTVYLDWI 266

RESULT 14
KFXHUI
coagulation factor Xia (EC 3.4.21.27) precursor [validated] - human
N;Alternate names: antihemophilic factor C; plasma thromboplastin antecedent
C;Species: Homo sapiens (man)
C;Date: 13-Aug-1986 #sequence_revision 26-May-1994 #text_change 09-Jul-2004
C;Accession: A27431; A00920; A37940
R;Asakai, R.; Davie, E.W.; Chung, D.W.
Biochemistry 26, 7221-7228, 1987
A;Title: Organization of the gene for human factor XI.
A;Reference numbers: A27431; MUID:88107663; PMID:2827746
A;Accession: A27431
A;Molecule type: DNA
A;Residues: 1-625 <ASA>
A;Cross-references: UNIPROT:P03951; GB:M18295
A;Note: the sequence shown follows the authors' translation
R;Fujikawa, K.; Chung, D.W.; Hendrickson, L.E.; Davie, E.W.
Biochemistry 25, 2417-2424, 1986
A;Title: Amino acid sequence of human factor XI, a blood coagulation factor with four tyrosine residues.
A;Reference numbers: A00920; MUID:86243360; PMID:3636155
A;Accession: A00920
A;Molecule type: mRNA
A;Residues: 1-625 <FUJ>
A;Cross-references: GB:M13142; NID:g182832; PIDN:AAA52487.1; PID:g182833
R;McMullen, B.A.; Fujikawa, K.; Davie, E.W.
Biochemistry 30, 2056-2060, 1991
A;Title: Location of the disulfide bonds in human coagulation factor XI: the presence of two interchain disulfide bonds.
A;Reference numbers: A37940; MUID:91152017; PMID:1998667
A;Accession: A37940
A;Molecule type: protein
A;Residues: 28-33;35-49, 'X', 51-55, 'X', 57-63;70-75, 'X', 77-79;107-109, 'X', 111-112;132-139, 'X', 141-142, 'X', 144-145, 'X', 147-148, 'X', 150-151, 'X', 153-154, 'X', 156-157, 'X', 159-160, 'X', 162-163, 'X', 165-166, 'X', 168-169, 'X', 171-172, 'X', 174-175, 'X', 177-178, 'X', 180-181, 'X', 183-184, 'X', 186-187, 'X', 189-190, 'X', 192-193, 'X', 195-196, 'X', 198-199, 'X', 201-202, 'X', 204-205, 'X', 207-208, 'X', 210-211, 'X', 213-214, 'X', 216-217, 'X', 219-220, 'X', 222-223, 'X', 225-226, 'X', 228-229, 'X', 231-232, 'X', 234-235, 'X', 237-238, 'X', 240-241, 'X', 243-244, 'X', 246-247, 'X', 249-250, 'X', 252-253, 'X', 255-256, 'X', 258-259, 'X', 261-262, 'X', 264-265, 'X', 267-268, 'X', 270-271, 'X', 273-274, 'X', 276-277, 'X', 279-280, 'X', 282-283, 'X', 285-286, 'X', 288-289, 'X', 291-292, 'X', 294-295, 'X', 297-298, 'X', 300-301, 'X', 303-304, 'X', 306-307, 'X', 309-310, 'X', 312-313, 'X', 315-316, 'X', 318-319;320-326, 'X', 328-330; 'X', 347-349;373, 'X', 375-376, 'X', 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Search completed: February 27, 2005, 20:23:27
Job time : 26.5815 secs

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OM protein - protein search, using sw model

Run on: February 27, 2005, 20:22:41 ; Search time 89.2843 Seconds
(without alignments)
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Title: US-10-040-647-6
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Scoring table: BLOSUM62
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Searched: 1385339 seqs, 32804528 residues

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Listing first 45 summaries

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7:	/cgn2_6/ptodata/1/pubaa/US08_NEW_PUB.pep.*
8:	/cgn2_6/ptodata/1/pubaa/US08_PUBCOMB.pep.*
9:	/cgn2_6/ptodata/1/pubaa/US09A_PUBCOMB.pep.*
10:	/cgn2_6/ptodata/1/pubaa/US09B_PUBCOMB.pep.*
11:	/cgn2_6/ptodata/1/pubaa/US09C_PUBCOMB.pep.*
12:	/cgn2_6/ptodata/1/pubaa/US09_NEW_PUB.pep.*
13:	/cgn2_6/ptodata/1/pubaa/US10A_PUBCOMB.pep.*
14:	/cgn2_6/ptodata/1/pubaa/US10B_PUBCOMB.pep.*
15:	/cgn2_6/ptodata/1/pubaa/US10C_PUBCOMB.pep.*
16:	/cgn2_6/ptodata/1/pubaa/US10D_PUBCOMB.pep.*
17:	/cgn2_6/ptodata/1/pubaa/US10_NEW_PUB.pep.*
18:	/cgn2_6/ptodata/1/pubaa/US11_NEW_PUB.pep.*
19:	/cgn2_6/ptodata/1/pubaa/US60_NEW_PUB.pep.*
20:	/cgn2_6/ptodata/1/pubaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1728	100.0	314	14	US-10-040-647-6
2	1723	99.7	314	9	US-09-968-415-3
3	1723	99.7	314	9	US-09-909-320-257
4	1723	99.7	314	9	US-09-885-441-14
5	1723	99.7	314	9	US-09-909-088B-257
6	1723	99.7	314	9	US-09-905-231A-257
7	1723	99.7	314	9	US-09-902-853-257
8	1723	99.7	314	9	US-09-907-824-257
9	1723	99.7	314	9	US-09-907-841-257
10	1723	99.7	314	10	US-09-904-011-257
11	1723	99.7	314	10	US-09-903-640-257
12	1723	99.7	314	10	US-09-908-093-257
13	1723	99.7	314	10	US-09-906-742-257

14	1723	99.7	314	10	US-09-906-838-257	Sequence 257, App
15	1723	99.7	314	10	US-09-907-613-257	Sequence 257, App
16	1723	99.7	314	10	US-09-907-942-257	Sequence 257, App
17	1723	99.7	314	10	US-09-904-859-257	Sequence 257, App
18	1723	99.7	314	10	US-09-909-204-257	Sequence 257, App
19	1723	99.7	314	10	US-09-904-820-257	Sequence 257, App
20	1723	99.7	314	10	US-09-904-786-257	Sequence 257, App
21	1723	99.7	314	10	US-09-906-646-257	Sequence 257, App
22	1723	99.7	314	10	US-09-906-780-257	Sequence 257, App
23	1723	99.7	314	10	US-09-903-786-257	Sequence 257, App
24	1723	99.7	314	10	US-09-902-903-257	Sequence 257, App
25	1723	99.7	314	10	US-09-903-749A-257	Sequence 257, App
26	1723	99.7	314	10	US-09-904-119-257	Sequence 257, App
27	1723	99.7	314	10	US-09-904-956-257	Sequence 257, App
28	1723	99.7	314	10	US-09-902-736-257	Sequence 257, App
29	1723	99.7	314	10	US-09-907-794-257	Sequence 257, App
30	1723	99.7	314	10	US-09-903-943-257	Sequence 257, App
31	1723	99.7	314	10	US-09-904-462-257	Sequence 257, App
32	1723	99.7	314	10	US-09-907-925-257	Sequence 257, App
33	1723	99.7	314	10	US-09-902-692-257	Sequence 257, App
34	1723	99.7	314	10	US-09-903-520-257	Sequence 257, App
35	1723	99.7	314	10	US-09-905-056-257	Sequence 257, App
36	1723	99.7	314	10	US-09-909-064-257	Sequence 257, App
37	1723	99.7	314	10	US-09-904-553-257	Sequence 257, App
38	1723	99.7	314	10	US-09-905-381-257	Sequence 257, App
39	1723	99.7	314	10	US-09-904-485-257	Sequence 257, App
40	1723	99.7	314	10	US-09-905-348-257	Sequence 257, App
41	1723	99.7	314	10	US-09-905-088-257	Sequence 257, App
42	1723	99.7	314	10	US-09-907-575-257	Sequence 257, App
43	1723	99.7	314	10	US-09-905-075-257	Sequence 257, App
44	1723	99.7	314	10	US-09-902-759-257	Sequence 257, App
45	1723	99.7	314	10	US-09-902-634-257	Sequence 257, App

ALIGNMENTS

RESULT 1
US-10-040-647-6
; Sequence 6, Application US/10040647
; Publication No. US20030092154A1
; GENERAL INFORMATION:
; APPLICANT: (US only) ANTALIS Toni Marie and HOOPER John David
; TITLE OF INVENTION: NOVEL MOLECULES
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/040,647
; FILING DATE: 07-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/023,942
; FILING DATE: <Unknown>
; APPLICATION NUMBER: P05101/97
; FILING DATE: 13-FEB-1997
; APPLICATION NUMBER: P0422/97
; FILING DATE: 18-NOV-1997
; APPLICATION NUMBER: International PCT Application
; FILING DATE: 13-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: DIGLIO, FRANK S
; REGISTRATION NUMBER: 31,346

REFERENCE/DOCKET NUMBER: 11168
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742 4343
TELEFAX: (516) 742 4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 314 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-040-647-6

Query Match 100.0%; Score 1728; DB 14; Length 314;
Best Local Similarity 100.0%; Pred. No. 3.7e-159;
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGARGALLALLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAEI GRWPMQGSRLR 60
DB 1 MGARGALLALLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAEI GRWPMQGSRLR 60

QY 61 LWDHSHVCGVSLLSHRWALTAACHCFETYSDLSDPGVMVQFGQLTSMPSFWSLQAYYTRYF 120
DB 61 LWDHSHVCGVSLLSHRWALTAACHCFETYSDLSDPGVMVQFGQLTSMPSFWSLQAYYTRYF 120

QY 121 VSNILSPRYLGNSPYDIALVKLSAPVYTKHIQICLOASTFEFENRTDCWVTGWGIYK 180
DB 121 VSNILSPRYLGNSPYDIALVKLSAPVYTKHIQICLOASTFEFENRTDCWVTGWGIYK 180

QY 181 EDEALPSPHTLQEQVVAIINNMCNHLFLKYSFRKIDFGDMVCAGNAQGGKACFGDSGG 240
DB 181 EDEALPSPHTLQEQVVAIINNMCNHLFLKYSFRKIDFGDMVCAGNAQGGKACFGDSGG 240

QY 241 PLACNKDGLWYQIGVSVGWGCGRPNRPGVYTNISHHFEWIKLMAQSGMSQDPDPSWPLL 300
DB 241 PLACNKDGLWYQIGVSVGWGCGRPNRPGVYTNISHHFEWIKLMAQSGMSQDPDPSWPLL 300

QY 301 FPELLWALPLGPV 314
DB 301 FPELLWALPLGPV 314

RESULT 2
US-09-968-415-3
Sequence 3, Application US/09968415
Publication No. US20020086334A1
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
Yue, Henry
Hillman, Jennifer L.
Guegler, Karl J.
Corley, Neil C.
Tang, Tom Y.
Shah, Purvi
TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/968,415
FILING DATE: 26-Sep-2001
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/659,151
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Mohan-Peterson, Sheela
REGISTRATION NUMBER: 41,201
REFERENCE/DOCKET NUMBER: PF-0458 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 314 amino acids
TYPE: amino acid
TOPOLOGY: linear
STRANDEDNESS: single
IMMEDIATE SOURCE:
LIBRARY: PROSTUT03
CLONE: 789927
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-968-415-3

Query Match 99.7%; Score 1723; DB 9; Length 314;
Best Local Similarity 99.7%; Pred. No. 1.1e-158;
Matches 313; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGARGALLALLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAEI GRWPMQGSRLR 60
DB 1 MGARGALLALLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAEI GRWPMQGSRLR 60

QY 61 LWDHSHVCGVSLLSHRWALTAACHCFETYSDLSDPGVMVQFGQLTSMPSFWSLQAYYTRYF 120
DB 61 LWDHSHVCGVSLLSHRWALTAACHCFETYSDLSDPGVMVQFGQLTSMPSFWSLQAYYTRYF 120

QY 121 VSNILSPRYLGNSPYDIALVKLSAPVYTKHIQICLOASTFEFENRTDCWVTGWGIYK 180
DB 121 VSNILSPRYLGNSPYDIALVKLSAPVYTKHIQICLOASTFEFENRTDCWVTGWGIYK 180

QY 181 EDEALPSPHTLQEQVVAIINNMCNHLFLKYSFRKIDFGDMVCAGNAQGGKACFGDSGG 240
DB 181 EDEALPSPHTLQEQVVAIINNMCNHLFLKYSFRKIDFGDMVCAGNAQGGKACFGDSGG 240

QY 241 PLACNKDGLWYQIGVSVGWGCGRPNRPGVYTNISHHFEWIKLMAQSGMSQDPDPSWPLL 300
DB 241 PLACNKDGLWYQIGVSVGWGCGRPNRPGVYTNISHHFEWIKLMAQSGMSQDPDPSWPLL 300

QY 301 FPELLWALPLGPV 314
DB 301 FPELLWALPLGPV 314

RESULT 3
US-09-909-320-257
Sequence 257, Application US/09909320
Patent No. US20020132240A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.

APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/909/320
PRIOR FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 257
LENGTH: 314
TYPE: PRT
ORGANISM: Homo Sapien
US-09-909-320-257

Query Match 99.7%; Score 1723; DB 9; Length 314;
Best Local Similarity 99.7%; Pred. No. 1.1e-158;
Matches 313; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGARGALLALLARAGLRKPESQEAAPLSGCGRRVITSRIVGEDAEALGRWPQGSRLR 60
DB 1 MGARGALLALLARAGLRKPESQEAAPLSGCGRRVITSRIVGEDAEALGRWPQGSRLR 60
QY 61 LWDHVCVSVLSLHRWALTAACHCFETYSDLSDPGCMVQFQQLTSMPSFWSLQAYTRYF 120
DB 61 LWDHVCVSVLSLHRWALTAACHCFETYSDLSDPGCMVQFQQLTSMPSFWSLQAYTRYF 120
QY 121 VSNLYLSPRYLGNPSYDIALVKLSAPVYTKHIQICLQASTFFENRTDCWVTGWGYIK 180
DB 121 VSNLYLSPRYLGNPSYDIALVKLSAPVYTKHIQICLQASTFFENRTDCWVTGWGYIK 180
QY 181 EDEALPSPHTLOEQVOVAIINNSMCNHLFLKYSFRKIDFGDMVCAGNAQGGKACFGDSGG 240
DB 181 EDEALPSPHTLOEQVOVAIINNSMCNHLFLKYSFRKIDFGDMVCAGNAQGGKACFGDSGG 240

QY 241 PLACNKDGLWYQIGVSWGVCGGRPNRPVGVYTNISHHFEWIKLMAQSGMSQPDPSWPLL 300
DB 241 PLACNKDGLWYQIGVSWGVCGGRPNRPVGVYTNISHHFEWIKLMAQSGMSQPDPSWPLL 300
QY 301 FFPLLWALPLLGPV 314
DB 301 FFPLLWALPLLGPV 314
RESULT 4
US-09-885-441-14
Sequence 14, Application US/09885441
Patent No. US20020146407A1
GENERAL INFORMATION:
APPLICANT: Xiao, Yonghong
TITLE OF INVENTION: Regulation of Human Eosinophil Serine
TITLE OF INVENTION: Protease-1-Like Enzyme
FILE REFERENCE: 04974.00512
CURRENT APPLICATION NUMBER: US/09/885,441
PRIOR FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: US 60/212,844
PRIOR FILING DATE: 2000-06-21
PRIOR APPLICATION NUMBER: US 60/244,171
PRIOR FILING DATE: 2000-10-31
PRIOR APPLICATION NUMBER: US 60/279,766
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: PCT/
PRIOR FILING DATE: 2001-06-20
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14
LENGTH: 314
TYPE: PRT
ORGANISM: Homo sapiens
US-09-885-441-14

Query Match 99.7%; Score 1723; DB 9; Length 314;
Best Local Similarity 99.7%; Pred. No. 1.1e-158;
Matches 313; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGARGALLALLARAGLRKPESQEAAPLSGCGRRVITSRIVGEDAEALGRWPQGSRLR 60
DB 1 MGARGALLALLARAGLRKPESQEAAPLSGCGRRVITSRIVGEDAEALGRWPQGSRLR 60
QY 61 LWDHVCVSVLSLHRWALTAACHCFETYSDLSDPGCMVQFQQLTSMPSFWSLQAYTRYF 120
DB 61 LWDHVCVSVLSLHRWALTAACHCFETYSDLSDPGCMVQFQQLTSMPSFWSLQAYTRYF 120
QY 121 VSNLYLSPRYLGNPSYDIALVKLSAPVYTKHIQICLQASTFFENRTDCWVTGWGYIK 180
DB 121 VSNLYLSPRYLGNPSYDIALVKLSAPVYTKHIQICLQASTFFENRTDCWVTGWGYIK 180
QY 181 EDEALPSPHTLOEQVOVAIINNSMCNHLFLKYSFRKIDFGDMVCAGNAQGGKACFGDSGG 240
DB 181 EDEALPSPHTLOEQVOVAIINNSMCNHLFLKYSFRKIDFGDMVCAGNAQGGKACFGDSGG 240
QY 241 PLACNKDGLWYQIGVSWGVCGGRPNRPVGVYTNISHHFEWIKLMAQSGMSQPDPSWPLL 300
DB 241 PLACNKDGLWYQIGVSWGVCGGRPNRPVGVYTNISHHFEWIKLMAQSGMSQPDPSWPLL 300
QY 301 FFPLLWALPLLGPV 314
DB 301 FFPLLWALPLLGPV 314

RESULT 5
US-09-909-088B-257
Sequence 257, Application US/09909088B
Patent No. US20020146709A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/909,088B
PRIOR FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 257
LENGTH: 314
TYPE: PRT
ORGANISM: Homo Sapien
US-09-909-088B-257

Query Match 99.7%; Score 1723; DB 9; Length 314;
Best Local Similarity 99.7%; Pred. No. 1.1e-158;
Matches 313; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGARGALLALLARAGLRKPESQEAAPLSGCGRRVITSRIVGGDAELGRNWPQGSRLR 60

Db 1 MGARGALLALLARAGLRKPESQEAAPLSGCGRRVITSRIVGGDAELGRNWPQGSRLR 60
QY 61 LWDSHVCGVSLSHRWALTAHCFETYSDLSDSGWMVQFQGLTSMPSFWSLQAYTRYF 120
Db 61 LWDSHVCGVSLSHRWALTAHCFETYSDLSDSGWMVQFQGLTSMPSFWSLQAYTRYF 120
QY 121 VSNYILSPRYLGNSPYDIALVKLSAPVTVTKHIQPICLQASTFEFENRTDCWVTGWYIK 180
Db 121 VSNYILSPRYLGNSPYDIALVKLSAPVTVTKHIQPICLQASTFEFENRTDCWVTGWYIK 180
QY 181 EDEALSPHTLOEVQVAIINNMCNHLFLKYSRDKIFGDMVCAGNAQGGKDACFGDSGG 240
Db 181 EDEALSPHTLOEVQVAIINNMCNHLFLKYSRDKIFGDMVCAGNAQGGKDACFGDSGG 240
QY 241 PLACNKDGLWYQIGVTVSWGVGCGRRNRPVTVTKHIQPICLQASTFEFENRTDCWVTGWYIK 300
Db 241 PLACNKDGLWYQIGVTVSWGVGCGRRNRPVTVTKHIQPICLQASTFEFENRTDCWVTGWYIK 300
QY 301 FPELLWALPLLPV 314
Db 301 FPELLWALPLLPV 314

RESULT 6
US-09-905-291A-257
Sequence 257, Application US/09905291A
Patent No. US20020160374A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/905,291A
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15

;; PRIOR APPLICATION NUMBER: PCT/US99/21547
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/23089
;; PRIOR FILING DATE: 1999-10-05
;; PRIOR APPLICATION NUMBER: PCT/US99/28214
;; PRIOR FILING DATE: 1999-11-29
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: 1999-11-30
;; PRIOR APPLICATION NUMBER: PCT/US99/28564
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/28565
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: 1999-12-16
;; PRIOR APPLICATION NUMBER: PCT/US99/30911
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US99/30999
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US00/00219
;; PRIOR FILING DATE: 2000-01-05
;; NUMBER OF SEQ ID NOS: 423
;; SEQ ID NO 257
;; LENGTH: 314
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-09-905-291A-257

Query Match 99.7%; Score 1723; DB 9; Length 314;
Best Local Similarity 99.7%; Pred. No. 1.1e-158;
Matches 313; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGARGALLALLARAGLRKPESQEAAPLSPGCGRRVITSRIVGGEAELGRWPQGSRLR 60
Db 1 MGARGALLALLARAGLRKPESQEAAPLSPGCGRRVITSRIVGGEAELGRWPQGSRLR 60

Qy 61 LWDHSVGVSLLSHRWALTAHCFETYSDLSDPGSMVQFQGLTSMPSFWSLQAYTRYF 120
Db 61 LWDHSVGVSLLSHRWALTAHCFETYSDLSDPGSMVQFQGLTSMPSFWSLQAYTRYF 120

Qy 121 VSNLYLSPRYLGNPSYDIALVKLSAPVYTYKHQIPICLOASTFFENRTDCWVTGWGIK 180
Db 121 VSNLYLSPRYLGNPSYDIALVKLSAPVYTYKHQIPICLOASTFFENRTDCWVTGWGIK 180

Qy 181 EDEALPSHTLQEQVAILINSMCNHFLKYSFRKIDFGDMVCAGNAGGKDACFGDSGG 240
Db 181 EDEALPSHTLQEQVAILINSMCNHFLKYSFRKIDFGDMVCAGNAGGKDACFGDSGG 240

Qy 241 PLACNKGWLWQIGVWSGVGCGRPNRPGVYTNISHHFEWIKLMAQSGMSQPPSPWPLL 300
Db 241 PLACNKGWLWQIGVWSGVGCGRPNRPGVYTNISHHFEWIKLMAQSGMSQPPSPWPLL 300

Qy 301 FFLMLWALPLGPV 314
Db 301 FFLMLWALPLGPV 314

RESULT 7
US-09-902-853-257
; Sequence 257, Application US/09902853
; Publication No. US20020192659A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary B.
; APPLICANT: Goddard, A.

;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, Christopher J.
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Hillan, Kenneth, J.
;; APPLICANT: KJavin, Ivar J.
;; APPLICANT: Mather, Jennie P.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William, I.
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: 10466-14
;; CURRENT APPLICATION NUMBER: US/09/902,853
;; CURRENT FILING DATE: 2001-07-10
;; PRIOR APPLICATION NUMBER: US/09/665,350
;; PRIOR FILING DATE: 2000-09-18
;; PRIOR APPLICATION NUMBER: US 60/143,048
;; PRIOR FILING DATE: 1999-07-07
;; PRIOR APPLICATION NUMBER: US 60/145,698
;; PRIOR FILING DATE: 1999-07-26
;; PRIOR APPLICATION NUMBER: US 60/146,222
;; PRIOR FILING DATE: 1999-07-28
;; PRIOR APPLICATION NUMBER: PCT/US99/20594
;; PRIOR FILING DATE: 1999-09-08
;; PRIOR APPLICATION NUMBER: PCT/US99/20944
;; PRIOR FILING DATE: 1999-09-13
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/21547
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/23089
;; PRIOR FILING DATE: 1999-10-05
;; PRIOR APPLICATION NUMBER: PCT/US99/28214
;; PRIOR FILING DATE: 1999-11-29
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: 1999-11-30
;; PRIOR APPLICATION NUMBER: PCT/US99/28564
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/28565
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: 1999-12-16
;; PRIOR APPLICATION NUMBER: PCT/US99/30911
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US99/30999
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US00/00219
;; PRIOR FILING DATE: 2000-01-05
;; NUMBER OF SEQ ID NOS: 423
;; SEQ ID NO 257
;; LENGTH: 314
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-09-902-853-257

Query Match 99.7%; Score 1723; DB 9; Length 314;
Best Local Similarity 99.7%; Pred. No. 1.1e-158;
Matches 313; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGARGALLALLARAGLRKPESQEAAPLSPGCGRRVITSRIVGGEAELGRWPQGSRLR 60
Db 1 MGARGALLALLARAGLRKPESQEAAPLSPGCGRRVITSRIVGGEAELGRWPQGSRLR 60

Qy 61 LWDHSVGVSLLSHRWALTAHCFETYSDLSDPGSMVQFQGLTSMPSFWSLQAYTRYF 120
Db 61 LWDHSVGVSLLSHRWALTAHCFETYSDLSDPGSMVQFQGLTSMPSFWSLQAYTRYF 120

Qy 121 VSNLYLSPRYLGNPSYDIALVKLSAPVYTYKHQIPICLOASTFFENRTDCWVTGWGIK 180

Db 121 VSNILSPRYLGNPYDIALVKLSAPVYTKHIQPICLOASTFEFENRTDCWVTGMYIK 180
QY 181 EDEALPSPHTLQEQVQVAIINNSMCNHLFLKYSFRKIDFGDMVCAGNAQGGKDACFGDSGG 240
Db 181 EDEALPSPHTLQEQVQVAIINNSMCNHLFLKYSFRKIDFGDMVCAGNAQGGKDACFGDSGG 240
QY 241 PLACNKDGLWYQIGVSWGCGRPNRPVYTNISHHFEWTKLMAQSGMSQDPSPWPLL 300
Db 241 PLACNKGLWYQIGVSWGCGRPNRPVYTNISHHFEWTKLMAQSGMSQDPSPWPLL 300
QY 301 FFPLLWALPLLPV 314
Db 301 FFPLLWALPLLPV 314

RESULT 8
US-09-907-824-257
; Sequence 257, Application US/09907824
; Publication No. US20020197671A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,824
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313

; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 257
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-907-824-257

Query Match 99.7%; Score 1723; DB 9; Length 314;
Best Local Similarity 99.7%; Pred. No. 1.le-158;
Matches 313; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGARGALLALLARAGLRKPEQEAAPLSGPCRRVITSRIVGGEDAELGRWPWQSLR 60
Db 1 MGARGALLALLARAGLRKPEQEAAPLSGPCRRVITSRIVGGEDAELGRWPWQSLR 60
QY 61 LWDSHVCGVSLLSHRWALTAHCFETYSDLSDPGMMVQFGOLTSMPFSWLSQAYTRYF 120
Db 61 LWDSHVCGVSLLSHRWALTAHCFETYSDLSDPGMMVQFGOLTSMPFSWLSQAYTRYF 120
QY 121 VSNILSPRYLGNPYDIALVKLSAPVYTKHIQPICLOASTFEFENRTDCWVTGMYIK 180
Db 121 VSNILSPRYLGNPYDIALVKLSAPVYTKHIQPICLOASTFEFENRTDCWVTGMYIK 180
QY 181 EDEALPSPHTLQEQVQVAIINNSMCNHLFLKYSFRKIDFGDMVCAGNAQGGKDACFGDSGG 240
Db 181 EDEALPSPHTLQEQVQVAIINNSMCNHLFLKYSFRKIDFGDMVCAGNAQGGKDACFGDSGG 240
QY 241 PLACNKDGLWYQIGVSWGCGRPNRPVYTNISHHFEWTKLMAQSGMSQDPSPWPLL 300
Db 241 PLACNKGLWYQIGVSWGCGRPNRPVYTNISHHFEWTKLMAQSGMSQDPSPWPLL 300
QY 301 FFPLLWALPLLPV 314
Db 301 FFPLLWALPLLPV 314

RESULT 9
US-09-907-841-257
; Sequence 257, Application US/09907841
; Publication No. US20020198366A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James

```

; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,841
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 257
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-907-841-257

Query Match          99.7%; Score 1723; DB 9; Length 314;
Best Local Similarity 99.7%; Pred. No. 1.1e-158;
Matches 313; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGARGALLALLARAGLRKPESQEAAPLSPGCGRRVITSRIVGDEAELGRWPQGSRLR 60
Db 1 MGARGALLALLARAGLRKPESQEAAPLSPGCGRRVITSRIVGDEAELGRWPQGSRLR 60
Qy 61 LWDHVCVSLLSHRWALTAACHCFETYSDLSDPGSMVQFQGLTSMPSFWSLQAYYTRYF 120
Db 61 LWDHVCVSLLSHRWALTAACHCFETYSDLSDPGSMVQFQGLTSMPSFWSLQAYYTRYF 120
Qy 121 VSNLYLSPRYLGNSPYDIALVKLSAPVTTYTHIQICLQASTFEFENRTDCWVTGWGVIK 180
Db 121 VSNLYLSPRYLGNSPYDIALVKLSAPVTTYTHIQICLQASTFEFENRTDCWVTGWGVIK 180
Qy 181 EDEALPSHTLQEVQVAIINNSMCHLFLKYSFRKIDFGDMVCAGNAQGGKDACFGHSGG 240
Db 181 EDEALPSHTLQEVQVAIINNSMCHLFLKYSFRKIDFGDMVCAGNAQGGKDACFGHSGG 240
Qy 241 PLACNKGWLWQIGVWSGVGCGRRNRPQGVYTNISHPFEWTKLMAQSGMSQDPSPWPLL 300
Db 241 PLACNKGWLWQIGVWSGVGCGRRNRPQGVYTNISHPFEWTKLMAQSGMSQDPSPWPLL 300
Qy 301 FFLLLWALPLIGPV 314
Db 301 FFLLLWALPLIGPV 314

RESULT 10
US-09-904-011-257
; Sequence 257, Application US/09904011
; Publication No. US2003000350A1
; GENERAL INFORMATION:
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Query Match 99.7%; Score 1723; DB 10; Length 314;
Best Local Similarity 99.7%; Pred. No. 1.le-158;
Matches 313; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGARGALLALLARAGLRKPEQEAAPLSGPCGRRVITSRIVGGDAELGRWPWQGSLLR 60
DB 1 MGARGALLALLARAGLRKPEQEAAPLSGPCGRRVITSRIVGGDAELGRWPWQGSLLR 60

QY 61 LWDHVCVSLLSHRWALTAHCFETVSDLSDPGMMVQFQGLTSMPSFWSLQAYYTRYF 120
DB 61 LWDHVCVSLLSHRWALTAHCFETVSDLSDPGMMVQFQGLTSMPSFWSLQAYYTRYF 120

QY 121 VSNYLSPRYLGNSPYDIALVKLSAPVYTKHIQICLQASTFEFENRTDCWVTGMYIK 180
DB 121 VSNYLSPRYLGNSPYDIALVKLSAPVYTKHIQICLQASTFEFENRTDCWVTGMYIK 180

QY 181 EDEALPSHTLOEQVQVAIINNSMCNHLFLKYSFRKDFGDMVCAGNAQGGKDACFGDSGG 240
DB 181 EDEALPSHTLOEQVQVAIINNSMCNHLFLKYSFRKDFGDMVCAGNAQGGKDACFGDSGG 240

QY 241 PLACNKDGLWYQIGVSVGWGCGRRPNRPGVYTNISHHFEMIQKMAQSGMSQDPSPWPLL 300
DB 241 PLACNKDGLWYQIGVSVGWGCGRRPNRPGVYTNISHHFEMIQKMAQSGMSQDPSPWPLL 300

QY 301 FFPLLWALPLLPV 314
DB 301 FFPLLWALPLLPV 314

RESULT 11
US-09-903-640-257
; Sequence 257, Application US/09903640
; Publication No. US20030017463A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/903,640
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 257
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-903-640-257

Query Match 99.7%; Score 1723; DB 10; Length 314;
Best Local Similarity 99.7%; Pred. No. 1.le-158;
Matches 313; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGARGALLALLARAGLRKPEQEAAPLSGPCGRRVITSRIVGGDAELGRWPWQGSLLR 60
DB 1 MGARGALLALLARAGLRKPEQEAAPLSGPCGRRVITSRIVGGDAELGRWPWQGSLLR 60

QY 61 LWDHVCVSLLSHRWALTAHCFETVSDLSDPGMMVQFQGLTSMPSFWSLQAYYTRYF 120
DB 61 LWDHVCVSLLSHRWALTAHCFETVSDLSDPGMMVQFQGLTSMPSFWSLQAYYTRYF 120

QY 121 VSNYLSPRYLGNSPYDIALVKLSAPVYTKHIQICLQASTFEFENRTDCWVTGMYIK 180
DB 121 VSNYLSPRYLGNSPYDIALVKLSAPVYTKHIQICLQASTFEFENRTDCWVTGMYIK 180

QY 181 EDEALPSHTLOEQVQVAIINNSMCNHLFLKYSFRKDFGDMVCAGNAQGGKDACFGDSGG 240
DB 181 EDEALPSHTLOEQVQVAIINNSMCNHLFLKYSFRKDFGDMVCAGNAQGGKDACFGDSGG 240

QY 241 PLACNKDGLWYQIGVSVGWGCGRRPNRPGVYTNISHHFEMIQKMAQSGMSQDPSPWPLL 300
DB 241 PLACNKDGLWYQIGVSVGWGCGRRPNRPGVYTNISHHFEMIQKMAQSGMSQDPSPWPLL 300

QY 301 FFPLLWALPLLPV 314
DB 301 FFPLLWALPLLPV 314

RESULT 12
US-09-908-093-257
; Sequence 257, Application US/09908093
; Publication No. US20030017498A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/908,093
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222

Db 1 MGARGALLALLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEAEELGRWPWGSLR 60
QY 61 LWDHSHVCGVSLSHRWALTAHCFETYSDLSDPGMMVQFGOLTSMPSPFSLQAYTRYF 120
Db 61 LWDHSHVCGVSLSHRWALTAHCFETYSDLSDPGMMVQFGOLTSMPSPFSLQAYTRYF 120
QY 121 VSNILSPRYLGNSPYDIALVKLSAPVYTKHQPICLQASTFEFENRTDCWVTGWGYIK 180
Db 121 VSNILSPRYLGNSPYDIALVKLSAPVYTKHQPICLQASTFEFENRTDCWVTGWGYIK 180
QY 181 EDEALPSPHTLQEVQVAIINNMCNHLFLKYSFRKDI FGMVCAAGNAQGGKDACFGDSGG 240
Db 181 EDEALPSPHTLQEVQVAIINNMCNHLFLKYSFRKDI FGMVCAAGNAQGGKDACFGDSGG 240
QY 241 PLACNKDGLWYQIGVSWGCGRRPNRPGVYTNISHHFEWIKLMAQSGMSQDPSPWPLL 300
Db 241 PLACNKDGLWYQIGVSWGCGRRPNRPGVYTNISHHFEWIKLMAQSGMSQDPSPWPLL 300
QY 301 FFPLLWALPLIGPV 314
Db 301 FFPLLWALPLIGPV 314

RESULT 14

US-09-906-838-257
; Sequence 257, Application US/09906838
; Publication No. US20030027143A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,838
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13

; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 257
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-906-838-257
Query Match 99.7%; Score 1723; DB 10; Length 314;
Best Local Similarity 99.7%; Pred. No. 1.1e-158;
Matches 313; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGARGALLALLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEAEELGRWPWGSLR 60
Db 1 MGARGALLALLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEAEELGRWPWGSLR 60
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Db 61 LWDHSHVCGVSLSHRWALTAHCFETYSDLSDPGMMVQFGOLTSMPSPFSLQAYTRYF 120
QY 121 VSNILSPRYLGNSPYDIALVKLSAPVYTKHQPICLQASTFEFENRTDCWVTGWGYIK 180
Db 121 VSNILSPRYLGNSPYDIALVKLSAPVYTKHQPICLQASTFEFENRTDCWVTGWGYIK 180
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Db 181 EDEALPSPHTLQEVQVAIINNMCNHLFLKYSFRKDI FGMVCAAGNAQGGKDACFGDSGG 240
QY 241 PLACNKDGLWYQIGVSWGCGRRPNRPGVYTNISHHFEWIKLMAQSGMSQDPSPWPLL 300
Db 241 PLACNKDGLWYQIGVSWGCGRRPNRPGVYTNISHHFEWIKLMAQSGMSQDPSPWPLL 300
QY 301 FFPLLWALPLIGPV 314
Db 301 FFPLLWALPLIGPV 314
RESULT 15
US-09-907-613-257
; Sequence 257, Application US/09907613
; Publication No. US20030027145A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tunas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,613
PRIOR FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 257
LENGTH: 314
TYPE: PRT
ORGANISM: Homo Sapien

Query Match 99.7%; Score 1723; DB 10; Length 314;
Best Local Similarity 99.7%; Pred. No. 1.1e-158;
Matches 313; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGARGALLALLARAGLRKPESQAAFLSGPCGRRVITSRIVGCEDAELGRWPQGSRLR 60
Db 1 MGARGALLALLARAGLRKPESQAAFLSGPCGRRVITSRIVGCEDAELGRWPQGSRLR 60
Qy 61 LWDSHVCGVLSLHRWALTAAHCFETYSDLSDPSCGMVQFGQLTSMPSFWSLQAYTRYF 120
Db 61 LWDSHVCGVLSLHRWALTAAHCFETYSDLSDPSCGMVQFGQLTSMPSFWSLQAYTRYF 120

Qy 121 VSNIIYLSPRYLGNSPYDIALVKLSAPVYTKHIQPICLQASTFEFENRTDCWVTGWGYIK 180
Db 121 VSNIIYLSPRYLGNSPYDIALVKLSAPVYTKHIQPICLQASTFEFENRTDCWVTGWGYIK 180
Qy 181 EDEALPSPHTLQEVQVAIINNSMCNHLFLKYSFRKQIFGDMVCAGNAQGGKDACFGDSGG 240
Db 181 EDEALPSPHTLQEVQVAIINNSMCNHLFLKYSFRKQIFGDMVCAGNAQGGKDACFGDSGG 240
Qy 241 PLACNKDGLWYQIGVWSWGVCGGRPNRPVYTTWISHHFEWIKLMAQSGMSQPPDSWPLL 300
Db 241 PLACNKDGLWYQIGVWSWGVCGGRPNRPVYTTWISHHFEWIKLMAQSGMSQPPDSWPLL 300
Qy 301 FFPLLWALPLLGPV 314
Db 301 FFPLLWALPLLGPV 314

Search completed: February 27, 2005, 20:39:49
Job time : 90.2843 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 27, 2005, 20:12:15 ; Search time 30.0958 Seconds
(without alignments)
778.839 Million cell updates/sec

Title: US-10-040-647-6

Perfect score: 1728

Sequence: 1 MGARGALLALLARAGLRK.....PSWLLFFPLLMALPLGPV 314

Scoring table: BLOSUM62

Gapex 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA.*
- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
 - 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
 - 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
 - 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
 - 5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*
 - 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1728	100.0	314	4	US-09-023-942A-6
2	1723	99.7	314	3	US-09-008-271A-3
3	1723	99.7	314	4	US-09-907-794A-257
4	1723	99.7	314	4	US-09-905-125A-257
5	1723	99.7	314	4	US-09-902-775A-257
6	1723	99.7	314	4	US-09-906-700-257
7	1723	99.7	314	4	US-09-903-603A-257
8	1723	99.7	314	4	US-09-904-920A-257
9	1723	99.7	314	4	US-09-909-064-257
10	1723	99.7	314	4	US-09-905-381A-257
11	1723	99.7	314	4	US-09-906-618-257
12	1706	98.7	312	4	US-09-023-942A-4
13	1414	81.8	306	4	US-09-386-642-53
14	1113.5	64.4	285	4	US-09-023-942A-26
15	573	33.2	290	4	US-09-386-653A-7
16	556	32.2	299	3	US-08-944-483-66
17	549	31.8	315	4	US-09-386-653A-9
18	543.5	31.5	328	4	US-09-386-642-11
19	542.5	31.4	319	4	US-09-386-642-12
20	536.5	31.0	317	4	US-09-386-629-7
21	536.5	31.0	317	4	US-09-907-794A-263
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24	536.5	31.0	317	4	US-09-906-700-263
25	536.5	31.0	317	4	US-09-903-603A-263
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27	536.5	31.0	317	4	US-09-909-064-263

28	536.5	31.0	317	4	US-09-905-381A-263	Sequence 263, App
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30	523.5	30.3	270	2	US-08-978-404B-8	Sequence 8, Appli
31	511.5	29.6	273	2	US-08-978-404B-6	Sequence 6, Appli
32	511	29.6	276	2	US-09-016-366A-15	Sequence 15, Appl
33	511	29.6	276	2	US-08-978-404B-21	Sequence 21, Appl
34	511	29.6	327	4	US-09-386-629-8	Sequence 8, Appli
35	510	29.5	273	2	US-09-016-366A-19	Sequence 19, Appl
36	510	29.5	273	2	US-08-978-404B-14	Sequence 14, Appl
37	510	29.5	638	2	US-08-681-151-3	Sequence 3, Appli
38	509	29.5	273	2	US-08-978-404B-3	Sequence 3, Appli
39	509	29.5	274	2	US-09-016-366A-21	Sequence 21, Appl
40	509	29.5	274	2	US-08-978-404B-16	Sequence 16, Appl
41	508.5	29.4	446	4	US-10-177-661-4	Sequence 4, Appli
42	508.5	29.4	477	4	US-10-177-661-2	Sequence 2, Appli
43	508.5	29.4	562	4	US-09-879-792-12	Sequence 12, Appl
44	507	29.3	267	2	US-09-016-366A-23	Sequence 23, Appl
45	507	29.3	267	2	US-08-978-404B-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-09-023-942A-6
; Sequence 6, Application US/09023942A
; Patent No. 6479274
; GENERAL INFORMATION:
; APPLICANT: (US only) ANTALIS Toni Marie and HOOPER John David
; TITLE OF INVENTION: NOVEL MOLECULES
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,942A
; FILING DATE: 13-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: POS101/97
; FILING DATE: 13-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PP0422/97
; FILING DATE: 18-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: International PCT Application
; FILING DATE: 13-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: DIGILIO, FRANK S
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 11169
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742 4343
; TELEFAX: (516) 742 4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 314 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-023-942A-6

Query Match 100.0%; Score 1728; DB 4; Length 314;

Best Local Similarity 100.0%; Pred. No. 1.1e-165;
Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGARGALLALLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAEIGRWPQGSRLR 60
DB 1 MGARGALLALLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAEIGRWPQGSRLR 60

QY 61 LWDHSHVCGVSLSHRWALTAHCFETYSDLSDPGMMVQFGLTSMPSFWSLQAYTRYF 120
DB 61 LWDHSHVCGVSLSHRWALTAHCFETYSDLSDPGMMVQFGLTSMPSFWSLQAYTRYF 120

QY 121 VSNIIYLSPRYLGNPSYDIALVKLSAPVYTKHIQPICLQASTFEFENRTDCWVTGWGYYK 180
DB 121 VSNIIYLSPRYLGNPSYDIALVKLSAPVYTKHIQPICLQASTFEFENRTDCWVTGWGYYK 180

QY 181 EDEALPSPHLTQEVQVAIIINNSMCNHLFLKYSFRKDI FGDWVCAGNAQGGKDACFGDSGG 240
DB 181 EDEALPSPHLTQEVQVAIIINNSMCNHLFLKYSFRKDI FGDWVCAGNAQGGKDACFGDSGG 240

QY 241 PLACNKDGLWYQIGVSVGWGCGRPNRPGVYTNISHHFEWIOKLMAQSGMSQDPPSWPLL 300
DB 241 PLACNKDGLWYQIGVSVGWGCGRPNRPGVYTNISHHFEWIOKLMAQSGMSQDPPSWPLL 300

QY 301 FPELLWALPLLGPV 314
DB 301 FPELLWALPLLGPV 314

RESULT 2
US-09-008-271A-3
; Sequence 3, Application US/09008271A
; Patent No. 6203979
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; Hillman, Jennifer L.
; Yue, Henry
; Guegler, Karl J.
; Corley, Neil C.
; Tang, Tom Y.
; Shah, Purvi.
; TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/008,271A
; FILING DATE: 16-Jan-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mohan-Peterson, Sheela
; REGISTRATION NUMBER: 41,201
; REFERENCE/DOCKET NUMBER: PF-0458 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 314 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

IMMEDIATE SOURCE:
LIBRARY: PROSTUT03
CLONE: 789927
SEQUENCE DESCRIPTION: SEQ ID NO: 3 :
US-09-008-271A-3

Query Match 99.7%; Score 1723; DB 3; Length 314;
Best Local Similarity 99.7%; Pred. No. 3.5e-165;
Matches 313; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGARGALLALLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAEIGRWPQGSRLR 60
DB 1 MGARGALLALLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAEIGRWPQGSRLR 60

QY 61 LWDHSHVCGVSLSHRWALTAHCFETYSDLSDPGMMVQFGLTSMPSFWSLQAYTRYF 120
DB 61 LWDHSHVCGVSLSHRWALTAHCFETYSDLSDPGMMVQFGLTSMPSFWSLQAYTRYF 120

QY 121 VSNIIYLSPRYLGNPSYDIALVKLSAPVYTKHIQPICLQASTFEFENRTDCWVTGWGYYK 180
DB 121 VSNIIYLSPRYLGNPSYDIALVKLSAPVYTKHIQPICLQASTFEFENRTDCWVTGWGYYK 180

QY 181 EDEALPSPHLTQEVQVAIIINNSMCNHLFLKYSFRKDI FGDWVCAGNAQGGKDACFGDSGG 240
DB 181 EDEALPSPHLTQEVQVAIIINNSMCNHLFLKYSFRKDI FGDWVCAGNAQGGKDACFGDSGG 240

QY 241 PLACNKDGLWYQIGVSVGWGCGRPNRPGVYTNISHHFEWIOKLMAQSGMSQDPPSWPLL 300
DB 241 PLACNKDGLWYQIGVSVGWGCGRPNRPGVYTNISHHFEWIOKLMAQSGMSQDPPSWPLL 300

QY 301 FPELLWALPLLGPV 314
DB 301 FPELLWALPLLGPV 314

RESULT 3
US-09-907-794A-257
; Sequence 257, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048

;; PRIOR FILING DATE: 1999-07-07
;; PRIOR APPLICATION NUMBER: US 60/145,698
;; PRIOR FILING DATE: 1999-07-26
;; PRIOR APPLICATION NUMBER: US 60/146,222
;; PRIOR FILING DATE: 1999-07-28
;; PRIOR APPLICATION NUMBER: PCT/US99/20594
;; PRIOR FILING DATE: 1999-09-08
;; PRIOR APPLICATION NUMBER: PCT/US99/20944
;; PRIOR FILING DATE: 1999-09-13
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/21547
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/23089
;; PRIOR FILING DATE: 1999-10-05
;; PRIOR APPLICATION NUMBER: PCT/US99/28214
;; PRIOR FILING DATE: 1999-11-29
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: 1999-11-30
;; PRIOR APPLICATION NUMBER: PCT/US99/28564
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/28565
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: 1999-12-16
;; PRIOR APPLICATION NUMBER: PCT/US99/30911
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US99/30999
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US00/00219
;; PRIOR FILING DATE: 2000-01-05
;; NUMBER OF SEQ ID NOS: 423
;; SEQ ID NO 257
;; LENGTH: 314
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-09-907-794A-257

Query Match 99.7%; Score 1723; DB 4; Length 314;
Best Local Similarity 99.7%; Pred. No. 3.5e-165;
Matches 313; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MGARGALLALLARAGLRKPESQEAAPLSPGCGRRVITSRIVGGEAEALGRWPQGSRLR	60
Db	1	MGARGALLALLARAGLRKPESQEAAPLSPGCGRRVITSRIVGGEAEALGRWPQGSRLR	60
Qy	61	LWDSHVCVSLSHRWALTAACFPETYSDLSDPGMMVQFQGLTSMPSFSLQAYTYRYF	120
Db	61	LWDSHVCVSLSHRWALTAACFPETYSDLSDPGMMVQFQGLTSMPSFSLQAYTYRYF	120
Qy	121	VSNTYLSPRYLGNSPYDIALVKLSAPVYTYKHQIPICLOASTFEFENRTDCWVTGWGYIK	180
Db	121	VSNTYLSPRYLGNSPYDIALVKLSAPVYTYKHQIPICLOASTFEFENRTDCWVTGWGYIK	180
Qy	181	EDEALPSHTLQVQVVAIINSMCNHLFLKYSFKDIFGDMVCAGNAQGGKDACFGDSGG	240
Db	181	EDEALPSHTLQVQVVAIINSMCNHLFLKYSFKDIFGDMVCAGNAQGGKDACFGDSGG	240
Qy	241	PLACNKGWLWQIGVWSGVCGRPNRGVYTNISHHFEWIKLMAQSGMSQDPSPWPLL	300
Db	241	PLACNKGWLWQIGVWSGVCGRPNRGVYTNISHHFEWIKLMAQSGMSQDPSPWPLL	300
Qy	301	FFPLLWALPLGPV 314	
Db	301	FFPLLWALPLGPV 314	

RESULT 4
US-09-905-125A-257
; Sequence 257, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.

;; APPLICANT: Ashkenazi, Avi
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Filvaroff, Ellen
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gao, Wei-Qiang
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, A.
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, Christopher J.
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Hillan, Kenneth, J.
;; APPLICANT: KJavin, Ivar J.
;; APPLICANT: Mather, Jennie P.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William, I.
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; TITLE OF INVENTION: Acids Encoding the Same
;; FILE REFERENCE: 10466-14
;; CURRENT APPLICATION NUMBER: US/09/905,125A
;; CURRENT FILING DATE: 2001-07-12
;; PRIOR APPLICATION NUMBER: PCT/US00/04414
;; PRIOR FILING DATE: 2000-02-22
;; PRIOR APPLICATION NUMBER: US 60/143,048
;; PRIOR FILING DATE: 1999-07-07
;; PRIOR APPLICATION NUMBER: US 60/145,698
;; PRIOR FILING DATE: 1999-07-26
;; PRIOR APPLICATION NUMBER: US 60/146,222
;; PRIOR FILING DATE: 1999-07-28
;; PRIOR APPLICATION NUMBER: PCT/US99/20594
;; PRIOR FILING DATE: 1999-09-08
;; PRIOR APPLICATION NUMBER: PCT/US99/20944
;; PRIOR FILING DATE: 1999-09-13
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/21547
;; PRIOR FILING DATE: 1999-09-15
;; PRIOR APPLICATION NUMBER: PCT/US99/23089
;; PRIOR FILING DATE: 1999-10-05
;; PRIOR APPLICATION NUMBER: PCT/US99/28214
;; PRIOR FILING DATE: 1999-11-29
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: 1999-11-30
;; PRIOR APPLICATION NUMBER: PCT/US99/28564
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/28565
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: 1999-12-16
;; PRIOR APPLICATION NUMBER: PCT/US99/30911
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US99/30999
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US00/00219
;; PRIOR FILING DATE: 2000-01-05
;; NUMBER OF SEQ ID NOS: 423
;; SEQ ID NO 257
;; LENGTH: 314
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-09-905-125A-257

Query Match 99.7%; Score 1723; DB 4; Length 314;
Best Local Similarity 99.7%; Pred. No. 3.5e-165;
Matches 313; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGARGALLALLARAGLRKPESQEAAPLSGPGCRRVITSRIVGGEDAEIAGRWPQGSRLR 60
Db 1 MGARGALLALLARAGLRKPESQEAAPLSGPGCRRVITSRIVGGEDAEIAGRWPQGSRLR 60
Qy 61 LWDSHVCGVSLLSHRWALTAHCFETYSDDLSDPSGWMVQFGLTSMPSFSLQAYTRYF 120
Db 61 LWDSHVCGVSLLSHRWALTAHCFETYSDDLSDPSGWMVQFGLTSMPSFSLQAYTRYF 120
Qy 121 VSNILSPRYLGNSPYDIALVKLSAPVYTKHQIPICLOASTFEFENRTDCWVTGWGYYK 180
Db 121 VSNILSPRYLGNSPYDIALVKLSAPVYTKHQIPICLOASTFEFENRTDCWVTGWGYYK 180
Qy 181 EDEALSPHTLQEVQVAIINNSMCNHLFLKYSPRKDIFGDMVCAGNAQGGKDACFGDSGG 240
Db 181 EDEALSPHTLQEVQVAIINNSMCNHLFLKYSPRKDIFGDMVCAGNAQGGKDACFGDSGG 240
Qy 241 PLACNKDGLWYQIGVSVGWGCGRPNRPVYTNISHHFEWIKLMAQSGMSQDPSPWPLL 300
Db 241 PLACNKDGLWYQIGVSVGWGCGRPNRPVYTNISHHFEWIKLMAQSGMSQDPSPWPLL 300
Qy 301 FFPLLWALPLLGPV 314
Db 301 FFPLLWALPLLGPV 314

RESULT 5

US-09-902-775A-257
; Sequence 257, Application US/09902775A

; Patent No. 6686451

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Baton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, A.

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth, J.

; APPLICANT: Kijavin, Ivar J.

; APPLICANT: Mather, Jennie P.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William, I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: 10466-14

; CURRENT APPLICATION NUMBER: US/09/902,775A

; CURRENT FILING DATE: 2001-07-10

; PRIOR APPLICATION NUMBER: PCT/US00/04414

; PRIOR FILING DATE: 2000-02-22

; PRIOR APPLICATION NUMBER: US 60/143,048

; PRIOR FILING DATE: 1999-07-07

; PRIOR APPLICATION NUMBER: US 60/145,698

; PRIOR FILING DATE: 1999-07-26

; PRIOR APPLICATION NUMBER: US 60/146,222

; PRIOR FILING DATE: 1999-07-28

; PRIOR APPLICATION NUMBER: PCT/US99/20594

; PRIOR FILING DATE: 1999-09-08

; PRIOR APPLICATION NUMBER: PCT/US99/20944

; PRIOR FILING DATE: 1999-09-13

; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 257
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-902-775A-257

Query Match

Best Local Similarity 99.7%; Score 1723; DB 4; Length 314;

Matches 313; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGARGALLALLARAGLRKPESQEAAPLSGPGCRRVITSRIVGGEDAEIAGRWPQGSRLR 60
Db 1 MGARGALLALLARAGLRKPESQEAAPLSGPGCRRVITSRIVGGEDAEIAGRWPQGSRLR 60
Qy 61 LWDSHVCGVSLLSHRWALTAHCFETYSDDLSDPSGWMVQFGLTSMPSFSLQAYTRYF 120
Db 61 LWDSHVCGVSLLSHRWALTAHCFETYSDDLSDPSGWMVQFGLTSMPSFSLQAYTRYF 120
Qy 121 VSNILSPRYLGNSPYDIALVKLSAPVYTKHQIPICLOASTFEFENRTDCWVTGWGYYK 180
Db 121 VSNILSPRYLGNSPYDIALVKLSAPVYTKHQIPICLOASTFEFENRTDCWVTGWGYYK 180
Qy 181 EDEALSPHTLQEVQVAIINNSMCNHLFLKYSPRKDIFGDMVCAGNAQGGKDACFGDSGG 240
Db 181 EDEALSPHTLQEVQVAIINNSMCNHLFLKYSPRKDIFGDMVCAGNAQGGKDACFGDSGG 240
Qy 241 PLACNKDGLWYQIGVSVGWGCGRPNRPVYTNISHHFEWIKLMAQSGMSQDPSPWPLL 300
Db 241 PLACNKDGLWYQIGVSVGWGCGRPNRPVYTNISHHFEWIKLMAQSGMSQDPSPWPLL 300
Qy 301 FFPLLWALPLLGPV 314
Db 301 FFPLLWALPLLGPV 314

RESULT 6

US-09-906-700-257
; Sequence 257, Application US/09906700

; Patent No. 6723535

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Baton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/906,700
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-15
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 257
LENGTH: 314
TYPE: PRT
ORGANISM: Homo Sapien
US-09-906-700-257
Query Match 99.7%; Score 1723; DB 4; Length 314;
Best Local Similarity 99.7%; Pred. No. 3.5e-165;
Matches 313; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGARGALLALLRAGLRKPESQEAAPLSGCGRRVITSRIVGSGDAELGRWPQGSRLR 60
DB 1 MGARGALLALLRAGLRKPESQEAAPLSGCGRRVITSRIVGSGDAELGRWPQGSRLR 60
QY 61 LWDSHVCGVSLLSHRWALTAACFTYSDLSDPGGMVQFGQLTSMPSFWSLQAYTRYF 120
DB 61 LWDSHVCGVSLLSHRWALTAACFTYSDLSDPGGMVQFGQLTSMPSFWSLQAYTRYF 120

QY 121 VSNLYLSPRYLGNSPYDIALVKLSAPVYTKHIQIPICLQASTPFEFNTDCWVTGWYIK 180
DB 121 VSNLYLSPRYLGNSPYDIALVKLSAPVYTKHIQIPICLQASTPFEFNTDCWVTGWYIK 180
QY 181 EDEALPSPHTLQEVQVAIINNSMCNHLFLKYSFRKIDFGDMVCAGNAQGGKDACFGDSCG 240
DB 181 EDEALPSPHTLQEVQVAIINNSMCNHLFLKYSFRKIDFGDMVCAGNAQGGKDACFGDSCG 240
QY 241 PLACNKGLWYQIGVWSGVCGRPNRPGVYTNISHFENITOKLMAQSGMSQDPSPWPLL 300
DB 241 PLACNKGLWYQIGVWSGVCGRPNRPGVYTNISHFENITOKLMAQSGMSQDPSPWPLL 300
QY 301 FFPLLWALPLLGPV 314
DB 301 FFPLLWALPLLGPV 314
RESULT 7
US-09-903-603A-257
Sequence 257, Application US/09903603A
Patent No. 6767995
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: GNE.1618P2C12
CURRENT APPLICATION NUMBER: US/09/903,603A
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313

;; PRIOR FILING DATE: 1999-11-30
;; PRIOR APPLICATION NUMBER: PCT/US99/28564
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/28565
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: 1999-12-16
;; PRIOR APPLICATION NUMBER: PCT/US99/30911
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US99/30999
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US00/00219
;; PRIOR FILING DATE: 2000-01-05
;; NUMBER OF SEQ ID NOS: 423
;; SEQ ID NO 257
;; LENGTH: 314
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-09-903-603A-257

Query Match 99.7%; Score 1723; DB 4; Length 314;
Best Local Similarity 99.7%; Pred. No. 3.5e-165;
Matches 313; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGARGALLALLARAGLRKPESQEAAPLSPGCCRRVITSRIVGGEDAEILGRWPWGSLR 60
Db 1 MGARGALLALLARAGLRKPESQEAAPLSPGCCRRVITSRIVGGEDAEILGRWPWGSLR 60
Qy 61 LWDSHVCGVSLLSHRWALTAHCFETYSDLSDPGSMWVQGLTSMPSFWSLQAYTRYF 120
Db 61 LWDSHVCGVSLLSHRWALTAHCFETYSDLSDPGSMWVQGLTSMPSFWSLQAYTRYF 120
Qy 121 VSNYLSPRYLGNSPYDIALVKLSAPVYTKHIQPICLQASTFEFENRTDCWVTGWGYIK 180
Db 121 VSNYLSPRYLGNSPYDIALVKLSAPVYTKHIQPICLQASTFEFENRTDCWVTGWGYIK 180
Qy 181 EDEALPSPHLTQEVQVAIINNSMCHLFLKYSPRKDIFGDMVCAGNAQGGKDACFGDSGG 240
Db 181 EDEALPSPHLTQEVQVAIINNSMCHLFLKYSPRKDIFGDMVCAGNAQGGKDACFGDSGG 240
Qy 241 PLACNKDGLWYQIGVSWGCGCRPNRPVYTNISHHFEWIKLMAQSGMSQDPDPSPWLL 300
Db 241 PLACNKDGLWYQIGVSWGCGCRPNRPVYTNISHHFEWIKLMAQSGMSQDPDPSPWLL 300
Qy 301 FFPLLWALPLIGPV 314
Db 301 FFPLLWALPLIGPV 314

RESULT 8

US-09-904-920A-257
; Sequence 257, Application US/09904920A
; Patent No. 6806352
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Macher, Jennie P.
; APPLICANT: Pan, James

;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William, I.
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: 10466-14
;; CURRENT APPLICATION NUMBER: US/09/904,920A
;; CURRENT FILING DATE: 2001-07-13
;; PRIOR APPLICATION NUMBER: PCT/US00/04414
;; PRIOR FILING DATE: 2000-02-22
;; PRIOR APPLICATION NUMBER: US 60/143,048
;; PRIOR FILING DATE: 1999-07-07
;; PRIOR APPLICATION NUMBER: US 60/145,698
;; PRIOR FILING DATE: 1999-07-26
;; PRIOR APPLICATION NUMBER: US 60/146,222
;; PRIOR FILING DATE: 1999-07-28
;; PRIOR APPLICATION NUMBER: PCT/US99/20594
;; PRIOR FILING DATE: 1999-09-08
;; PRIOR APPLICATION NUMBER: PCT/US99/20944
;; PRIOR FILING DATE: 1999-09-13
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: 1999-09-15
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;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: 1999-11-30
;; PRIOR APPLICATION NUMBER: PCT/US99/28564
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/28565
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: 1999-12-16
;; PRIOR APPLICATION NUMBER: PCT/US99/30911
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US99/30999
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US00/00219
;; NUMBER OF SEQ ID NOS: 423
;; SEQ ID NO 257
;; LENGTH: 314
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-09-904-920A-257

Query Match 99.7%; Score 1723; DB 4; Length 314;
Best Local Similarity 99.7%; Pred. No. 3.5e-165;
Matches 313; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGARGALLALLARAGLRKPESQEAAPLSPGCCRRVITSRIVGGEDAEILGRWPWGSLR 60
Db 1 MGARGALLALLARAGLRKPESQEAAPLSPGCCRRVITSRIVGGEDAEILGRWPWGSLR 60
Qy 61 LWDSHVCGVSLLSHRWALTAHCFETYSDLSDPGSMWVQGLTSMPSFWSLQAYTRYF 120
Db 61 LWDSHVCGVSLLSHRWALTAHCFETYSDLSDPGSMWVQGLTSMPSFWSLQAYTRYF 120
Qy 121 VSNYLSPRYLGNSPYDIALVKLSAPVYTKHIQPICLQASTFEFENRTDCWVTGWGYIK 180
Db 121 VSNYLSPRYLGNSPYDIALVKLSAPVYTKHIQPICLQASTFEFENRTDCWVTGWGYIK 180
Qy 181 EDEALPSPHLTQEVQVAIINNSMCHLFLKYSPRKDIFGDMVCAGNAQGGKDACFGDSGG 240
Db 181 EDEALPSPHLTQEVQVAIINNSMCHLFLKYSPRKDIFGDMVCAGNAQGGKDACFGDSGG 240
Qy 241 PLACNKDGLWYQIGVSWGCGCRPNRPVYTNISHHFEWIKLMAQSGMSQDPDPSPWLL 300

Db 241 PLACNKGMLYQIGVSVGCGRPNRPVYTNISHHFEWIKLMAQSGMSQDPSPWPLL 300
Qy 301 FFPLLWALPLGPV 314
Db 301 FFPLLWALPLGPV 314

RESULT 9

US-09-909-064-257
; Sequence 257, Application US/09909064
; Patent No. 6818449
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,064
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
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; PRIOR FILING DATE: 1999-07-28
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; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20

; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 257
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-909-064-257

Query Match 99.7%; Score 1723; DB 4; Length 314;
Best Local Similarity 99.7%; Pred No. 3.5e-165;
Matches 313; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGARGALLALLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPQGSRLR 60
Db 1 MGARGALLALLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPQGSRLR 60

Qy 61 LWDSHVCGVSLLSHRWALTAACHCFETYSDLSDPSCGMVQFGLTSMPSFWSLQAYTRYF 120
Db 61 LWDSHVCGVSLLSHRWALTAACHCFETYSDLSDPSCGMVQFGLTSMPSFWSLQAYTRYF 120

Qy 121 VSNILSPRYLGNSPYDIALVLSAPVYTKHIQPICLQASTFEFENRTDCWVTGWIYK 180
Db 121 VSNILSPRYLGNSPYDIALVLSAPVYTKHIQPICLQASTFEFENRTDCWVTGWIYK 180

Qy 181 EDEALPSPHTLQEQVVAIINNSMCNHLFLKYSFRKIDFGDMVCAGNAQGGKACFGDSGG 240
Db 181 EDEALPSPHTLQEQVVAIINNSMCNHLFLKYSFRKIDFGDMVCAGNAQGGKACFGDSGG 240

Qy 241 PLACNKGMLYQIGVSVGCGRPNRPVYTNISHHFEWIKLMAQSGMSQDPSPWPLL 300
Db 241 PLACNKGMLYQIGVSVGCGRPNRPVYTNISHHFEWIKLMAQSGMSQDPSPWPLL 300

Qy 301 FFPLLWALPLGPV 314
Db 301 FFPLLWALPLGPV 314

RESULT 10
US-09-905-381A-257
; Sequence 257, Application US/09905381A
; Patent No. 6818746
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/905/381A
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 257
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-905-381A-257

Query Match 99.7%; Score 1723; DB 4; Length 314;
Best Local Similarity 99.7%; Pred. No. 3.5e-165;
Matches 313; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGARGALLLLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAEILGRWPWQGSRLR 60
Db 1 MGARGALLLLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAEILGRWPWQGSRLR 60
Qy 61 LWDSHVCGVSLSHRWALTAAHCFETYSDDLSDPSGMMVQFCOLTSMPFSWLSQAYTRYF 120
Db 61 LWDSHVCGVSLSHRWALTAAHCFETYSDDLSDPSGMMVQFCOLTSMPFSWLSQAYTRYF 120
Qy 121 VSNLYLSPRYLGNSPYDIALVKLSAPVYTKHIQPICLQASTFEFENRTDCWVTGWCYIK 180
Db 121 VSNLYLSPRYLGNSPYDIALVKLSAPVYTKHIQPICLQASTFEFENRTDCWVTGWCYIK 180
Qy 181 EDEALPSPHTLQEVQVAIINNSMCHLFLKYSFRKDI FGMVCMAGNAQGGKACFGDSGG 240
Db 181 EDEALPSPHTLQEVQVAIINNSMCHLFLKYSFRKDI FGMVCMAGNAQGGKACFGDSGG 240
Qy 241 PLACNKDGLWYQIGVSGWCGCRPNRPGVYTNISHHFEWTKLMAQSGMSQDDPSWPLL 300
Db 241 PLACNKDGLWYQIGVSGWCGCRPNRPGVYTNISHHFEWTKLMAQSGMSQDDPSWPLL 300
Qy 301 FFFLLWALPLIGPV 314
Db 301 FFFLLWALPLIGPV 314

RESULT 11

US-09-906-618-257
; Sequence 257, Application US/09906618
; Patent No. 6828146
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,618
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 257
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo Sapien

US-09-906-618-257

Query Match 99.7%; Score 1723; DB 4; Length 314;
Best Local Similarity 99.7%; Pred. No. 3.5e-165;
Matches 313; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGARGALLALLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEAEGLRWQGSRLR 60
DB 1 MGARGALLALLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEAEGLRWQGSRLR 60
QY 61 LWDHSHVCGVSLLSHRWALTAHCFETYSDLSDPGMMVQFQGLTSMPSFWSLQAYTRYF 120
DB 61 LWDHSHVCGVSLLSHRWALTAHCFETYSDLSDPGMMVQFQGLTSMPSFWSLQAYTRYF 120
QY 121 VSNITLSPRYLGNSPYDIALVKLSAPVYTKHIQIPICLOASTPFENRTDCWWTGMYIK 180
DB 121 VSNITLSPRYLGNSPYDIALVKLSAPVYTKHIQIPICLOASTPFENRTDCWWTGMYIK 180
QY 181 EDEALPSHTLOEVQVVAIINNSMCNHLFLKYSFRKIDFGDMVCAGNAQGGKACFGDSGG 240
DB 181 EDEALPSHTLOEVQVVAIINNSMCNHLFLKYSFRKIDFGDMVCAGNAQGGKACFGDSGG 240
QY 241 PLACNKDGLWYQIGVSWGVCGRPNRPVGTNTSHHFETIQKLMAQSGMSQDPSPWPLL 300
DB 241 PLACNKDGLWYQIGVSWGVCGRPNRPVGTNTSHHFETIQKLMAQSGMSQDPSPWPLL 300
QY 301 FFLMLWALPLGPV 314
DB 301 FFLMLWALPLGPV 314

RESULT 12

US-09-023-942A-4
Sequence 4, Application US/09023942A
Patent No. 6479274
GENERAL INFORMATION:
APPLICANT: (US only) ANTALIS Toni Marie and HOOPER John David
TITLE OF INVENTION: NOVEL MOLECULES
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 GARDEN CITY PLAZA
CITY: GARDEN CITY
STATE: NEW YORK
COUNTRY: USA
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.2.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,942A
FILING DATE: 13-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: POS101/97
FILING DATE: 13-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP0422/97
FILING DATE: 18-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: International PCT Application
FILING DATE: 13-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: DIGIGLIO, FRANK S
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 11168
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742 4343
TELEFAX: (516) 742 4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 312 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-023-942A-4
Query Match 98.7%; Score 1706; DB 4; Length 312;
Best Local Similarity 99.4%; Pred. No. 1.8e-163;
Matches 312; Conservative 0; Mismatches 0; Indels 2; Gaps 1;
QY 1 MGARGALLALLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEAEGLRWQGSRLR 60
DB 1 MGARGALLALLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEAEGLRWQGSRLR 60
QY 61 LWDHSHVCGVSLLSHRWALTAHCFETYSDLSDPGMMVQFQGLTSMPSFWSLQAYTRYF 120
DB 61 LWDHSHVCGVSLLSHRWALTAHCFETYSDLSDPGMMVQFQGLTSMPSFWSLQAYTRYF 120
QY 121 VSNITLSPRYLGNSPYDIALVKLSAPVYTKHIQIPICLOASTPFENRTDCWWTGMYIK 180
DB 121 VSNITLSPRYLGNSPYDIALVKLSAPVYTKHIQIPICLOASTPFENRTDCWWTGMYIK 178
QY 181 EDEALPSHTLOEVQVVAIINNSMCNHLFLKYSFRKIDFGDMVCAGNAQGGKACFGDSGG 240
DB 179 EDEALPSHTLOEVQVVAIINNSMCNHLFLKYSFRKIDFGDMVCAGNAQGGKACFGDSGG 238
QY 241 PLACNKDGLWYQIGVSWGVCGRPNRPVGTNTSHHFETIQKLMAQSGMSQDPSPWPLL 300
DB 239 PLACNKDGLWYQIGVSWGVCGRPNRPVGTNTSHHFETIQKLMAQSGMSQDPSPWPLL 298
QY 301 FFLMLWALPLGPV 314
DB 299 FFLMLWALPLGPV 312

RESULT 13

US-09-386-642-53
Sequence 53, Application US/09386642
Patent No. 6420157
GENERAL INFORMATION:
APPLICANT: Darrow, Andrew
APPLICANT: Qi, Jensen
APPLICANT: Andrade-Gordon, Patricia
TITLE OF INVENTION: Zymogen Activation System
FILE REFERENCE: ORT-1028
CURRENT APPLICATION NUMBER: US/09/386,642
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 53
LENGTH: 306
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Fusion gene of
OTHER INFORMATION: human protease F in CFEK2 zymogen vector
US-09-386-642-53
Query Match 81.8%; Score 1414; DB 4; Length 306;
Best Local Similarity 89.3%; Pred. No. 4.4e-134;
Matches 260; Conservative 5; Mismatches 20; Indels 6; Gaps 2;
QY 10 ALLARAGLRKP--ESQEAAPLSGPCGRRVITSRIVGGEAEGLRWQGSRLRWDSHV 66
DB 11 ALLGTFGCGVPDYKDDDAALAAPDD---DDKIVGGYALELGRWPQGSRLRWDSHV 67
QY 67 CGVSLLSHRWALTAHCFETYSDLSDPGMMVQFQGLTSMPSFWSLQAYTRYFVSNYL 126
DB 68 CGVSLLSHRWALTAHCFETYSDLSDPGMMVQFQGLTSMPSFWSLQAYTRYFVSNYL 127
QY 127 SPRYLGNSPYDIALVKLSAPVYTKHIQIPICLOASTPFENRTDCWWTGMYIKEDALP 186

Db 128 SPYLGNSPYDIALVKLSAPVYTKHIQICLOASTFEFENRTDCWVTGWGVIKEDEALP 187
QY 187 SPHTLQVQVAIIINNSMCNHLFLKYSPRKDI FGMVCAAGKQKDACFGDGGPLACNK 246
Db 188 SPHTLQVQVAIIINNSMCNHLFLKYSPRKDI FGMVCAAGKQKDACFGDGGPLACNK 247
QY 247 DGLWYQIGVSVGWGCGRPNRPVYTNISHHFEWIKLMAQSGMSQDPDSW 297
Db 248 NGLWYQIGVSVGWGCGRPNRPVYTNISHHFEWIKLMAQSGMSQDPDSW 298

RESULT 14

US-09-023-942A-26
; Sequence 26, Application US/09023942A
; Patent No. 6479274
; GENERAL INFORMATION:
; APPLICANT: (US only) ANTALIS Toni Marie and HOOPER John David
; TITLE OF INVENTION: NOVEL MOLECULES
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,942A
; FILING DATE: 13-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: POS101/97
; FILING DATE: 13-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PP0422/97
; FILING DATE: 18-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: International PCT Application
; FILING DATE: 13-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: DIGIGLIO, FRANK S
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 11168
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742 4343
; TELEFAX: (516) 742 4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 285 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-023-942A-26

Query Match 64.4%; Score 1113.5; DB 4; Length 285;
Best Local Similarity 69.1%; Pred. No. 7.3e-104;
Matches 197; Conservative 35; Mismatches 50; Indels 3; Gaps 2;
QY 29 LSGPCGRVITSIVGGEDAEELGWPHQSGSLRWDSHVCGVSLISHRWALTAACHCPTYS 88
Db 3 LSGPCGHRITPSRIYVGGDDAEELGWPHQSGSLRWVGNHLGATLLNRRVLTAAHCFQ--X 60
QY 89 DLSDPSGWMVQFGOLTSPGFSWLSQAYTRYFVSNYLSPYLGNSPYDIALVKLSAPVT 148
Db 61 D-NDPFDWTVQFGLTSRPSLWNLQAYSNRYQIEDIFLSPKYSEQYENDIALKLSFVT 119
QY 149 YTKHIQICLOASTFEFENRTDCWVTGWGVIKEDEALPSPHTLQEVQVAIIINNSMCNHLF 208

Db 120 YNNFIQIPICLLANSTYKFNRTDCWVTGWGAIGEDSLSPNTLQEVQVAIIINNSMCNHY 179
QY 209 LKYSREKDI FGMVCAAGKQKDACFGDGGPLACNKDGLWYQIGVSVGWGCGRPNRP 268
Db 180 KXPDFRTNIGWDMVCAAGTPEGKDACFGDGGPLACDQDTVWYQGVSVGWGCGRPNRP 239
QY 269 GYVTNISHHFEWIKLMAQSGMSQDPDSWPLFFPLLWALPLLP 313
Db 240 GYVTNISHHYNVIQSTWIRNGLLRPDPVPLLLFLTLAWASSLLRP 284

RESULT 15

US-09-386-653A-7
; Sequence 7, Application US/09386653A
; Patent No. 6458564
; GENERAL INFORMATION:
; APPLICANT: Andrade-Gordon, Patricia
; APPLICANT: Barrow, Andrew
; APPLICANT: Qi, Jian-shen
; TITLE OF INVENTION: DNA encoding the novel human serine
; FILE REFERENCE: ORT-1032
; CURRENT APPLICATION NUMBER: US/09/386,653A
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 7
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-386-653A-7

Query Match 33.2%; Score 573; DB 4; Length 290;
Best Local Similarity 42.6%; Pred. No. 2e-49;
Matches 123; Conservative 44; Mismatches 100; Indels 22; Gaps 8;
QY 4 RGALLALLARAGLRKPESQEAAPLSGPCGRRVITSIVGGEDAEELGRWPMQGSRLRLWD 63
Db 3 RPAAPVPLLLLLCFGSQRAKAATA-----CGRPMLNRWVGQDTQEGEWPQVSIQRNG 56
QY 64 SHVCGVSLISHRWALTAACHCFETYSDLSDPGWMVQFG--OLTSMPFSWLSQAYTRYFY 121
Db 57 SHFCGSLIAEQWLVLTAAHCFR---NTSETSLYQVLLGARQLVQP---GFHAMYAR--V 107
QY 122 SNIVLSPRYLGNSPYDIALVKLSAPVYTKHIQICLOASTFEFENRTDCWVTGWGVIK 180
Db 108 RQVESNPLYQGTASSADVALVEAPVPTNYILPVCLPDPSPVIFETGMNCWVTGWGSPS 167
QY 181 EDEALPSPHTLQEVQVAIIINNSMCNHLFLK---YSFR-KDIFGDMVCAGNAQGGKDACFG 236
Db 168 EEDLLPEPRILQKLAVPDIIDTPKCNLLYSKDTFEGYQPKTIKNDMLCAGFEKGKQACKG 227
QY 237 DSGGPLACNKDGLWYQIGVSVGWGCGRPNRPVYTNISHHFEWIKL 285
Db 228 DSGGPLVCLVQGSWLOAGVISGEGCARQNRPGVYIRVTAHNNWIIHRII 276

Search completed: February 27, 2005, 20:24:33
Job time : 31.0958 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 27, 2005, 20:03:40 ; Search time 117.374 Seconds
(without alignments)
1034.667 Million cell updates/sec

Title: US-10-040-647-6

Perfect score: 1728

Sequence: 1 MGARGALLALLARAGLRK.....PSWLLFFPLLNALLPGVP 314

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04.*

- 1: Geneseq1980s.*
- 2: Geneseq1990s.*
- 3: Geneseq2000s.*
- 4: Geneseq2001s.*
- 5: Geneseq2002s.*
- 6: Geneseq2003as.*
- 7: Geneseq2003bs.*
- 8: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1728	100.0	314	2 AAW77297	AAW77297 Amino aci
2	1723	99.7	314	2 AAW77296	AAW77296 Amino aci
3	1723	99.7	314	2 AAW97116	AAW97116 A human e
4	1723	99.7	314	2 AAY06434	AAY06434 Human pro
5	1723	99.7	314	2 AAY13388	AAY13388 Amino aci
6	1723	99.7	314	3 AAB12132	AAB12132 Hydrophob
7	1723	99.7	314	3 ADC78569	ADC78569 Human PRO
8	1723	99.7	314	4 AAB80256	AAB80256 Human PRO
9	1723	99.7	314	4 AAU02223	AAU02223 Human ext
10	1723	99.7	314	5 AAEL17010	AAEL17010 Human eos
11	1723	99.7	314	6 ABU71634	ABU71634 Human PRO
12	1723	99.7	314	6 ABU71489	ABU71489 Human PRO
13	1723	99.7	314	6 ABU71935	ABU71935 Human sec
14	1723	99.7	314	6 ABO01818	ABO01818 Novel hum
15	1723	99.7	314	6 ABUS4391	ABUS4391 Human sec
16	1723	99.7	314	6 ABO47406	ABO47406 Human sec
17	1723	99.7	314	6 ABU64543	ABU64543 Human sec
18	1723	99.7	314	6 ABU67389	ABU67389 Human sec
19	1723	99.7	314	6 ABO14909	ABO14909 Human sec
20	1723	99.7	314	6 ABU69666	ABU69666 Novel hum
21	1723	99.7	314	6 ABO14848	ABO14848 Human sec
22	1723	99.7	314	6 ADB29462	ADB29462 Human sec
23	1723	99.7	314	6 ADA18318	ADA18318 Human sec
24	1723	99.7	314	6 ABO32800	ABO32800 Human sec
25	1723	99.7	314	6 ABO34860	ABO34860 Human PRO

26	1723	99.7	314	6 ADA16293	Ada16293 Human sec
27	1723	99.7	314	6 ADA42438	Ada42438 Human sec
28	1723	99.7	314	6 ABO17538	ABO17538 Human PRO
29	1723	99.7	314	7 ADA16717	Ada16717 Human sec
30	1723	99.7	314	7 ADA13146	Ada13146 Human sec
31	1723	99.7	314	7 ADA42014	Ada42014 Human sec
32	1723	99.7	314	7 ADA17361	Ada17361 Human sec
33	1723	99.7	314	7 ADA42864	Ada42864 Human sec
34	1723	99.7	314	7 ABO17599	ABO17599 Human PRO
35	1723	99.7	314	7 ADB80572	ADB80572 Ovarian c
36	1723	99.7	314	7 ADB77783	ADB77783 Human sec
37	1723	99.7	314	7 ADB74919	ADB74919 Human sec
38	1723	99.7	314	7 ADC28565	ADC28565 Human sec
39	1723	99.7	314	7 ADC39765	ADC39765 Human sec
40	1723	99.7	314	7 ADC40279	ADC40279 Human sec
41	1723	99.7	314	7 ADC19103	ADC19103 Human sec
42	1723	99.7	314	7 ADC34403	ADC34403 Human sec
43	1723	99.7	314	7 ADC29458	ADC29458 Human sec
44	1723	99.7	314	7 ADC28989	ADC28989 Human sec
45	1723	99.7	314	7 ADC40874	ADC40874 Human sec

ALIGNMENTS

RESULT 1
AAW77297

ID AAW77297 standard; protein; 314 AA.

XX AAW77297;

XX AC AAW77297;

XX DT 07-JAN-1999 (first entry)

XX DE Amino acid sequence of long isoform of HELA2.

XX KW Serine protease; regulation; cell activity; viability; HELA2; ATC2;

XX KW BCOM3; testisin; fertility; suppressor; testicular germ cell cancer;

XX KW seminoma; testis-specific expression; antitumour; sperm development;

XX KW infertility.

XX OS Homo sapiens.

XX PN WO9836054-A1.

XX PD 20-AUG-1998.

XX PF 13-FEB-1998; 98WO-AUG000085.

XX PR 13-FEB-1997; 97AU-00005101.

XX PR 18-NOV-1997; 97AU-00000422.

XX PA (AMRA-) AMRAD OPERATIONS PTY LTD.

XX PI Antalis TM, Hooper JD;

XX XX WPI; 1998-480768/41.

XX DR N-PSDB; AAV59119.

XX XX New serine protease(s) and kinase involved in regulating cell activity

XX PT and viability - particularly the testis-specific protease HELA2 used for

XX PT modulation of fertility and as tumour suppressor.

XX XX Claim 3; Page 62-64; 167pp; English.

XX CC The present sequence represents the amino acid sequence of the long

XX CC isoform of HELA2. cDNA generated from HeLa cells and PAI-2 expressing

XX CC HeLa cells was amplified using PCR primers AAV48312-13. Three new

XX CC sequences were detected in the 480 bp amplicon. These sequences are

XX CC designated HELA2 and ATC2 which have high homology to serine proteases

XX CC and BCOM3 which has homology to a kinase. The proteins are involved in or

XX CC associated with regulation of cell activity and/or viability.

XX CC Administration of recombinant HELA2 (also called testisin) is used to

XX CC increase fertility. Downregulation of HELA2 reduces fertility. HELA2 is

CC also a suppressor of testicular germ cell cancers (seminoma) and is also
 CC expressed in some non-testicular cancers (of colon, pancreas, prostate
 CC and ovary), so is a marker/potential therapeutic target for cancer. The
 CC promoter from the HELA2 gene is useful for testis-specific expression of
 CC other genes, e.g. for gene therapy or modulation of fertility. Drugs that
 CC block activity of HELA2 should have antitumour activity (other than in
 CC testis) while in testis recombinant HELA2 should stop growth of tumours
 CC and normalise sperm development (eliminating the need for orchidectomy).
 CC Identification of mutant forms of HELA2 can be used to diagnose
 CC infertility
 XX

SQ Sequence 314 AA;

Query Match 100.0%; Score 1728; DB 2; Length 314;
 Best Local Similarity 100.0%; Pred. No. 5.9e-147;
 Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGARGALLALLARAGLRKPESQEAAPLSPGCGRRVITSRIYGGEDAEIGRWPWGSLR 60

DB 1 MGARGALLALLARAGLRKPESQEAAPLSPGCGRRVITSRIYGGEDAEIGRWPWGSLR 60

QY 61 LWDHSHVCGVSLLSHRWALTAACFETYSDDLSPSGMWVQFGLTSPFWSLQAYYTRYF 120

DB 61 LWDHSHVCGVSLLSHRWALTAACFETYSDDLSPSGMWVQFGLTSPFWSLQAYYTRYF 120

QY 121 VSNILSPRYLGNSPYDIALVKLSAPVYTKHQICLOASTFEFENRTDCWVTGWGYIK 180

DB 121 VSNILSPRYLGNSPYDIALVKLSAPVYTKHQICLOASTFEFENRTDCWVTGWGYIK 180

QY 181 EDEALPSPHTLQEVQVAIINNSMCNHLFLKYSFRKIDFGDMVCAGNAQGGKDACFGDSGG 240

DB 181 EDEALPSPHTLQEVQVAIINNSMCNHLFLKYSFRKIDFGDMVCAGNAQGGKDACFGDSGG 240

QY 241 PLACNKDGLWYQIGVSWGCGGRRPNRPVYTNISHHFEWIKLMAQSGMSQDPSPWPLL 300

DB 241 PLACNKDGLWYQIGVSWGCGGRRPNRPVYTNISHHFEWIKLMAQSGMSQDPSPWPLL 300

QY 301 FFPILLWALPLLGPV 314

DB 301 FFPILLWALPLLGPV 314

RESULT 2

AAW77296
 ID AAW77296 standard; protein; 314 AA.

AC AAW77296;

XX 07-JAN-1999 (first entry)

DE Amino acid sequence of the short isoform of HELA2.

XX Serine protease; regulation; cell activity; viability; HELA2; ATC2;
 KW BCOM3; testis; fertility; suppressor; testicular germ cell cancer;
 KW seminoma; testis-specific expression; antitumour; sperm development;
 KW infertility.

XX Homo sapiens.

XX WO9836054-A1.

XX 20-AUG-1998.

XX 13-FEB-1998; 98WO-AU0000085.

XX 13-FEB-1997; 97AU-00005101.

XX 18-NOV-1997; 97AU-00000422.

XX (AMRA-) AMRAD OPERATIONS PTY LTD.

XX Antalis TM, Hooper JD;

XX WPI; 1998-480768/41.

DR N-PSDB; AAV59118.

XX New serine protease(s) and kinase involved in regulating cell activity
 PT and viability - particularly the testis-specific protease HELA2 used for
 PT modulation of fertility and as tumour suppressor.

XX Claim 2; Fig 6; 167pp; English.

XX The present sequence represents the amino acid sequence of the short
 CC isoform of HELA2. cDNA generated from HeLa cells and PAI-2 expressing
 CC HeLa cells was amplified using PCR primers AAV48312-13. Three new
 CC sequences were detected in the 480 bp amplicon. These sequences are
 CC designated HELA2 and ATC2 which have high homology to serine proteases
 CC and BCOM3 which has homology to a kinase. The proteins are involved in or
 CC associated with regulation of cell activity and/or viability.

CC Administration of recombinant HELA2 (also called testin) is used to
 CC increase fertility. Downregulation of HELA2 reduces fertility. HELA2 is
 CC also a suppressor of testicular germ cell cancers (seminoma) and is also
 CC expressed in some non-testicular cancers (of colon, pancreas, prostate
 CC and ovary), so is a marker/potential therapeutic target for cancer. The
 CC promoter from the HELA2 gene is useful for testis-specific expression of
 CC other genes, e.g. for gene therapy or modulation of fertility. Drugs that
 CC block activity of HELA2 should have antitumour activity (other than in
 CC testis) while in testis recombinant HELA2 should stop growth of tumours
 CC and normalise sperm development (eliminating the need for orchidectomy).
 CC Identification of mutant forms of HELA2 can be used to diagnose
 CC infertility
 XX

SQ Sequence 314 AA;

Query Match 99.7%; Score 1723; DB 2; Length 314;

Best Local Similarity 99.7%; Pred. No. 1.7e-146;

Matches 313; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGARGALLALLARAGLRKPESQEAAPLSPGCGRRVITSRIYGGEDAEIGRWPWGSLR 60

DB 1 MGARGALLALLARAGLRKPESQEAAPLSPGCGRRVITSRIYGGEDAEIGRWPWGSLR 60

QY 61 LWDHSHVCGVSLLSHRWALTAACFETYSDDLSPSGMWVQFGLTSPFWSLQAYYTRYF 120

DB 61 LWDHSHVCGVSLLSHRWALTAACFETYSDDLSPSGMWVQFGLTSPFWSLQAYYTRYF 120

QY 121 VSNILSPRYLGNSPYDIALVKLSAPVYTKHQICLOASTFEFENRTDCWVTGWGYIK 180

DB 121 VSNILSPRYLGNSPYDIALVKLSAPVYTKHQICLOASTFEFENRTDCWVTGWGYIK 180

QY 181 EDEALPSPHTLQEVQVAIINNSMCNHLFLKYSFRKIDFGDMVCAGNAQGGKDACFGDSGG 240

DB 181 EDEALPSPHTLQEVQVAIINNSMCNHLFLKYSFRKIDFGDMVCAGNAQGGKDACFGDSGG 240

QY 241 PLACNKDGLWYQIGVSWGCGGRRPNRPVYTNISHHFEWIKLMAQSGMSQDPSPWPLL 300

DB 241 PLACNKDGLWYQIGVSWGCGGRRPNRPVYTNISHHFEWIKLMAQSGMSQDPSPWPLL 300

QY 301 FFPILLWALPLLGPV 314

DB 301 FFPILLWALPLLGPV 314

RESULT 3

AAW97116

ID AAW97116 standard; protein; 314 AA.

XX AAW97116;

XX 04-MAY-1999 (first entry)

DE A human eosinophil serine protease.

XX Human; eosinophil; serine protease; allergic disease; infectious disease;
 KW tumour; granulomatous disease; collagen disease; vascular inflammation.

XX Homo sapiens.

```
XX PN JP11032768-A.
XX PD 09-FEB-1999.
XX PF 16-JUL-1997; 97JP-00191319.
XX PR 16-JUL-1997; 97JP-00191319.
XX PA (ONOI ) ONO PHARM CO LTD.
XX WPI; 1999-183825/16.
XX N-PSDB; AAX15336.
XX
XX New eosinophils serine protease - useful for prevention and treatment of
XX allergic, infectious, tumor, granulomatous and collagen diseases.
XX
XX Claim 1; Page 9-10; 18pp; Japanese.
XX
XX The present sequence represents a human eosinophil serine protease. The
XX protease is useful in drug compositions for the prevention and treatment
XX of allergic diseases, infectious diseases, tumour diseases, granulomatous
XX diseases, collagen diseases and vascular inflammation
XX
XX Sequence 314 AA;
XX
XX Query Match 99.7%; Score 1723; DB 2; Length 314;
XX Best Local Similarity 99.7%; Pred. No. 1.7e-146;
XX Matches 313; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 1 MGARGALLALLARAGLRKPEQEAAPLSGPGCRRVITSRIVGDEAELGRWPQGSRLR 60
Db 1 MGARGALLALLARAGLRKPEQEAAPLSGPGCRRVITSRIVGDEAELGRWPQGSRLR 60
Qy 61 LWDSHVCGVSLSHRWALTAACHFETYSDLSDPSGMMVQFGQLTSMPSFWSLQAYTYRYF 120
Db 61 LWDSHVCGVSLSHRWALTAACHFETYSDLSDPSGMMVQFGQLTSMPSFWSLQAYTYRYF 120
Qy 121 VSNITLSPRYLGNSPYDIALVKLSAPVYTKHIQICLQASTFFENRTDCWVTGWDYIK 180
Db 121 VSNITLSPRYLGNSPYDIALVKLSAPVYTKHIQICLQASTFFENRTDCWVTGWDYIK 180
Qy 181 EDEALPSPHTLOEQVQVAILNNSMCHLFLKYSFRKIDFGDMVCAGNAQGGKACFGDSGG 240
Db 181 EDEALPSPHTLOEQVQVAILNNSMCHLFLKYSFRKIDFGDMVCAGNAQGGKACFGDSGG 240
Qy 241 PLACNKDGLWTQIGVWSGVCGCPNRPVGTNTSHHFEWIKLMAQSGMSQPPDSWPLL 300
Db 241 PLACNKDGLWTQIGVWSGVCGCPNRPVGTNTSHHFEWIKLMAQSGMSQPPDSWPLL 300
Qy 301 FFLPLWALPLLPV 314
Db 301 FFLPLWALPLLPV 314
RESULT 4
AAY06434
ID AAY06434 standard; protein; 314 AA.
AC AAY06434;
XX
XX 27-SEP-1999 (first entry)
XX Human protease HUPM-3.
XX
XX Protease; human; HUPM-3; cell proliferation; cancer; immune disorder;
XX inflammation; therapy.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..19
XX /note= "putative signal peptide"
```

```
FT Protein 20..314
FT Modified-site /note= "putative mature protein"
FT Modified-site 39 /note= "protein kinase C phosphorylation site"
FT Modified-site 58 /note= "protein kinase C phosphorylation site"
FT Modified-site 73 /note= "protein kinase C phosphorylation site"
FT Active-site 82 /note= "protein kinase C phosphorylation site"
FT Modified-site 86 /note= "casein kinase II phosphorylation site"
FT Modified-site 127 /note= "protein kinase C phosphorylation site"
FT Modified-site 134 /note= "casein kinase II phosphorylation site"
FT Modified-site 161 /note= "casein kinase II phosphorylation site"
FT Modified-site 167 /note= "casein kinase II phosphorylation site"
FT Modified-site 190 /note= "N-glycosylated"
FT Modified-site 200 /note= "casein kinase II phosphorylation site"
FT Modified-site 212 /note= "N-glycosylated"
FT Active-site 238 /note= "protein kinase C phosphorylation site"
FT Modified-site 273 /note= "N-glycosylated"
FT Modified-site 291 /note= "casein kinase II phosphorylation site"
XX
XX W09936550-A2.
XX
XX 22-JUL-1999.
XX
XX 12-JAN-1999; 99WO-US0000655.
XX
XX 16-JAN-1998; 98US-00008271.
XX (INCY-) INCYTE PHARM INC.
XX
XX Bandman O, Hillman JL, Yue H, Guegler KJ, Corley NC, Tang YT;
XX Shan F;
XX
XX WPI; 1999-430616/36.
XX N-PSDB; AAX87151.
XX
XX Novel human protease molecules useful in the treatment of developmental
XX disorders and/or cancers.
XX
XX Claim 1; Page 71-72; 90pp; English.
XX
XX The present sequence represents novel human protease HUPM-3, as deduced
XX from the consensus sequence (see AAX87151) of overlapping cDNA clones
XX obtained from various libraries. Northern analysis shows expression of
XX HUPM-3 in cardiovascular, haematopoietic and male reproductive cDNA
XX libraries. Approximately 86% of these libraries are associated with
XX neoplastic disorders. The invention provides 12 new human proteases, i.e.
XX HUPM-1 to -12 (see AAY06432-43), and the polynucleotides encoding them
XX (see AAX87149-60). Also provided are vectors, host cells and methods for
XX producing HUPM polypeptides, as well as agonists and antagonists of HUPM.
XX Methods for treating or preventing cell proliferative disorders and
XX immune disorders using HUPM or HUPM antagonists are claimed
XX
XX Sequence 314 AA;
XX
XX Query Match 99.7%; Score 1723; DB 2; Length 314;
XX Best Local Similarity 99.7%; Pred. No. 1.7e-146;
XX Matches 313; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 1 MGARGALLALLARAGLRKPEQEAAPLSGPGCRRVITSRIVGDEAELGRWPQGSRLR 60
Db 1 MGARGALLALLARAGLRKPEQEAAPLSGPGCRRVITSRIVGDEAELGRWPQGSRLR 60
```

Qy 61 LWDHVGCVSLSHRWALTAHCFETYSDLSDPGMMVQFGOLTSMPFSWLSQAYTRYF 120
 Db 61 LWDHVGCVSLSHRWALTAHCFETYSDLSDPGMMVQFGOLTSMPFSWLSQAYTRYF 120
 Qy 121 VSNLYLSPRYLGNFPIALVKLSAPVYTYKHIOPICLQASTFEFENRTDCWVTGWGYIK 180
 Db 121 VSNLYLSPRYLGNFPIALVKLSAPVYTYKHIOPICLQASTFEFENRTDCWVTGWGYIK 180
 Qy 181 EDEALPSHTLOEVQVAILNNSMCHLFLKYSFRKIDFGDMVCAGNAOGKDAFCGDSGG 240
 Db 181 EDEALPSHTLOEVQVAILNNSMCHLFLKYSFRKIDFGDMVCAGNAOGKDAFCGDSGG 240
 Qy 241 PLACNKDGLWYQIGVSWGCGRPNRPVGVYTNISHHFETIKLMAQSGMSQDPSPWPLL 300
 Db 241 PLACNKGLMWYQIGVSWGCGRPNRPVGVYTNISHHFETIKLMAQSGMSQDPSPWPLL 300
 Qy 301 FFPILLWALPLIGPV 314
 Db 301 FFPILLWALPLIGPV 314
 RESULT 5
 AAY13388
 ID AAY13388 standard; protein; 314 AA.
 AC AAY13388;
 AC AAY13388;
 DT 25-JUN-1999 (first entry)
 DE Amino acid sequence of protein PRO303.
 KW Secreted protein; transmembrane protein; human; enterocolitis;
 KW Zollinger-Ellison syndrome; gastrointestinal ulceration;
 KW congenital microvillus atrophy; skin disease; cell growth;
 KW abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
 KW Parkinson's disease; Alzheimer's disease; ALS; neuropathy; fibromodulin;
 KW dermal scarring; Usher Syndrome; Atrophla areata; anti-thrombotic;
 KW wound healing; tissue repair.
 XX Homo sapiens.
 OS Homo sapiens.
 XX WO9914328-A2.
 XX 25-MAR-1999.
 XX 16-SEP-1998; 98WO-US019330.
 XX 17-SEP-1997; 97US-0059113P.
 XX 17-SEP-1997; 97US-0059115P.
 XX 17-SEP-1997; 97US-0059117P.
 XX 17-SEP-1997; 97US-0059119P.
 XX 17-SEP-1997; 97US-0059121P.
 XX 17-SEP-1997; 97US-0059122P.
 XX 17-SEP-1997; 97US-0059184P.
 XX 18-SEP-1997; 97US-0059263P.
 XX 18-SEP-1997; 97US-0059266P.
 XX 15-OCT-1997; 97US-0062125P.
 XX 17-OCT-1997; 97US-0062285P.
 XX 17-OCT-1997; 97US-0062287P.
 XX 21-OCT-1997; 97US-0063486P.
 XX 24-OCT-1997; 97US-0062814P.
 XX 24-OCT-1997; 97US-0063127P.
 XX 24-OCT-1997; 97US-0063045P.
 XX 24-OCT-1997; 97US-0063120P.
 XX 24-OCT-1997; 97US-0063121P.
 XX 24-OCT-1997; 97US-0063122P.
 XX 27-OCT-1997; 97US-0063327P.
 XX 27-OCT-1997; 97US-0063329P.
 XX 28-OCT-1997; 97US-0063541P.
 XX 28-OCT-1997; 97US-0063542P.
 XX 28-OCT-1997; 97US-0063544P.

PR 28-OCT-1997; 97US-0063549P.
 PR 28-OCT-1997; 97US-0063550P.
 PR 28-OCT-1997; 97US-0063554P.
 PR 29-OCT-1997; 97US-0063435P.
 PR 29-OCT-1997; 97US-0063704P.
 PR 29-OCT-1997; 97US-0063732P.
 PR 29-OCT-1997; 97US-0063734P.
 PR 29-OCT-1997; 97US-0063735P.
 PR 29-OCT-1997; 97US-0063738P.
 PR 29-OCT-1997; 97US-0064215P.
 PR 31-OCT-1997; 97US-0063870P.
 PR 31-OCT-1997; 97US-0064103P.
 PR 03-NOV-1997; 97US-0064248P.
 PR 07-NOV-1997; 97US-0064809P.
 PR 12-NOV-1997; 97US-0065186P.
 PR 17-NOV-1997; 97US-0065846P.
 PR 18-NOV-1997; 97US-0065693P.
 PR 21-NOV-1997; 97US-0066120P.
 PR 21-NOV-1997; 97US-0066364P.
 PR 24-NOV-1997; 97US-0066453P.
 PR 24-NOV-1997; 97US-0066466P.
 PR 24-NOV-1997; 97US-0066511P.
 PR 24-NOV-1997; 97US-0066770P.
 PR 24-NOV-1997; 97US-0066772P.
 PR 25-NOV-1997; 97US-0066840P.
 XX (GETH) GENENTECH INC.
 PA Wood WI, Gurney AL, Goddard A, Pennica D, Chen J, Yuan J;
 XX WPI; 1999-229533/19.
 DR N-PSDB; AAX52259.
 XX New isolated human genes and polypeptides used in, e.g. treatment of
 PT gastrointestinal ulceration.
 XX Claim 12; Fig 92; 320pp; English.
 CC AAY1344-403 represent secreted and transmembrane human proteins. The
 CC cDNA sequences are obtained from cDNA libraries, prepared from fetal
 CC lung, fetal kidney, fetal brain, fetal liver and fetal retina. The
 CC encoded polypeptides have specific uses based on their homology to known
 CC polypeptides, e.g. PRO211 and PRO217 can be used for disorders associated
 CC with the preservation and maintenance of gastrointestinal mucosa and the
 CC repair of acute and chronic mucosal lesions (e.g. enterocolitis,
 CC Zollinger-Ellison syndrome, gastrointestinal ulceration and congenital
 CC microvillus atrophy), skin diseases associated with abnormal keratinocyte
 CC differentiation (e.g. psoriasis, epithelial cancers such as lung squamous
 CC cell carcinoma of the vulva and gliomas), potent effects on cell growth
 CC and development, diseases related to growth or survival of nerve cells
 CC including Parkinson's disease, Alzheimer's disease, ALS, neuropathies or
 CC cancer. PRO265 can be used as for fibromodulin, e.g. for reducing dermal
 CC scarring. PRO264 can be used as a target for anti-tumor drugs. PRO533 may
 CC be used in the treatment of Usher Syndrome or Atrophla areata; PRO269 can
 CC be used as an anti-thrombotic agent; PRO287 polypeptides and portions may
 CC have therapeutic applications in wound healing and tissue repair; PRO317
 CC can be used for treating problems of the kidney, uterus, endometrium,
 CC blood vessels, or related tissue, e.g. in the heart of genital tract
 XX Sequence 314 AA;
 SQ
 Query Match 99.7%; Score 1723; DB 2; Length 314;
 Best Local Similarity 99.7%; Pred. No. 1.7e-146;
 Matches 313; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MGARGALLALLIARAGLRKPSQEAAPLSPGCGRRVITSRIVGGDAELGRWPGQSLR 60
 Db 1 MGARGALLALLIARAGLRKPSQEAAPLSPGCGRRVITSRIVGGDAELGRWPGQSLR 60
 Qy 61 LWDHVGCVSLSHRWALTAHCFETYSDLSPPSGMMVQFGOLTSMPFSWLSQAYTRYF 120
 Db 61 LWDHVGCVSLSHRWALTAHCFETYSDLSPPSGMMVQFGOLTSMPFSWLSQAYTRYF 120

QY 121 VSNILSPRYLGNSPYDIALVKLSAPVYTKHIQIPICLOASTFEFENRTDCWVTGWGVIK 180
Db 121 VSNILSPRYLGNSPYDIALVKLSAPVYTKHIQIPICLOASTFEFENRTDCWVTGWGVIK 180
QY 181 EDEALPSPHTLQEVQVAIINNMCNHLFLKYSFRKIDFGDMVCAGNAQGGKDACFGDSGG 240
Db 181 EDEALPSPHTLQEVQVAIINNMCNHLFLKYSFRKIDFGDMVCAGNAQGGKDACFGDSGG 240
QY 241 PLACNKDGLWYQIGVWSGCGRPNRPVYTNISHHFEWTKLMAQSGMSQPPSPWPLL 300
Db 241 PLACNKGLWYQIGVWSGCGRPNRPVYTNISHHFEWTKLMAQSGMSQPPSPWPLL 300
QY 301 FFPLLWALPLIGPV 314
Db 301 FFPLLWALPLIGPV 314

RESULT 6
AAB12132
ID AAB12132 standard; protein; 314 AA.
XX AC AAB12132;
XX DT 02-FEB-2001 (first entry)
XX DE Hydrophobic domain protein from clone HP03116 isolated from KB cells.
XX KW Human; secreted protein; membrane protein; hydrophobic domain;
KW proliferation control; differentiation induction; material transport;
KW biophylaxis; signal receptor; ion channel; transporter; immunostimulant;
KW immunosuppressant; haematopoiesis regulator; chemotactic; chemokinetic;
KW haemostatic; thrombolytic; anti-inflammatory; tumour inhibition;
KW autoimmune disease; Alzheimer's disease; Parkinson's disease; cancer.
XX OS Homo sapiens.
XX PN WO200029448-A2.
XX PD 25-MAY-2000.
XX PF 17-NOV-1999; 99WO-JP006412.
XX PR 17-NOV-1998; 98JP-00326255.
XX PR 22-DEC-1998; 98JP-00364315.
XX PR 16-MAR-1999; 99JP-00069811.
XX PR 27-APR-1999; 99JP-00119299.
XX PR 19-MAY-1999; 99JP-00138169.
XX PA (SAGA) SAGAMI CHEM RES CENT.
XX PA (PROT-) PROTEGENE INC.
XX PI Kato S, Kimura T;
XX WPI; 2000-387753/33.
XX DR N-FSD; AAA62005, AAA62015.
XX PT Proteins comprising hydrophobic regions, such as secretory and membrane
PT proteins, useful in research and diagnostics and having various
PT activities e.g. immunomodulatory, antiinflammatory, chemokinetic,
PT hemostatic, thrombolytic.
XX PS Claim 1; Page 238-240; 410pp; English.
XX CC Secretory proteins play important roles in the proliferation control, the
CC differentiation induction, the material transport and the biophylaxis of
CC cells. Membrane proteins have important roles as signal receptors, ion
CC channels and transporters. The present sequence is a human protein which
CC has at least one hydrophobic domain. This protein may be a secretory or a
CC membrane protein. The present protein may have cytokine and cell
CC proliferation/differentiation activity, immune stimulating or suppressing
CC activity, haematopoiesis activity, tissue growth activity,
CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, anti-inflammatory activity and tumour

CC inhibition activity. The present protein could therefore be used for
CC treatment of autoimmune disease, Alzheimer's disease, Parkinson's
XX disease, and cancer
XX SQ Sequence 314 AA;
Query Match 99.7%; Score 1723; DB 3; Length 314;
Best Local Similarity 99.7%; Pred. No. 1.7e-146;
Matches 313; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGARGALLALLARAGLRKPESQEAAPLSPGCGRRVITTSRIVGDEAELGRWPQGSRLR 60
Db 1 MGARGALLALLARAGLRKPESQEAAPLSPGCGRRVITTSRIVGDEAELGRWPQGSRLR 60
QY 61 LWDHSVGVSLLSHRWALTAACFCETYSDDLSDPSGMVQFGLTSMPSFWSLQAYYTRYF 120
Db 61 LWDHSVGVSLLSHRWALTAACFCETYSDDLSDPSGMVQFGLTSMPSFWSLQAYYTRYF 120
QY 121 VSNILSPRYLGNSPYDIALVKLSAPVYTKHIQIPICLOASTFEFENRTDCWVTGWGVIK 180
Db 121 VSNILSPRYLGNSPYDIALVKLSAPVYTKHIQIPICLOASTFEFENRTDCWVTGWGVIK 180
QY 181 EDEALPSPHTLQEVQVAIINNMCNHLFLKYSFRKIDFGDMVCAGNAQGGKDACFGDSGG 240
Db 181 EDEALPSPHTLQEVQVAIINNMCNHLFLKYSFRKIDFGDMVCAGNAQGGKDACFGDSGG 240
QY 241 PLACNKDGLWYQIGVWSGCGRPNRPVYTNISHHFEWTKLMAQSGMSQPPSPWPLL 300
Db 241 PLACNKGLWYQIGVWSGCGRPNRPVYTNISHHFEWTKLMAQSGMSQPPSPWPLL 300
QY 301 FFPLLWALPLIGPV 314
Db 301 FFPLLWALPLIGPV 314

RESULT 7
ADC78569
ID ADC78569 standard; protein; 314 AA.
XX AC ADC78569;
XX DT 01-JAN-2004 (first entry)
XX DE Human PRO303 protein.
XX KW antiinflammatory; antiulcer; cytostatic; antipsoriatic; antiparkinsonian;
KW neutropic; neuroprotective; vasotropic; chemotactic; angiogenic;
KW neurotrophic; osteopathic; antiasthmatic; antiarthritic; antirheumatic;
KW antiarteriosclerotic; cardiant; antidiabetic; cerebroprotective;
KW thrombolytic; immunomodulator; enterocolitis; Zollinger-Ellison syndrome;
KW gastrointestinal ulceration; psoriasis; cancer; Parkinson's disease;
KW Alzheimer's; ALS; neuropathy; dermal scarring; wound healing;
KW nerve repair; thrombosis; bone; cartilage formation; angiogenesis;
KW asthma; rheumatoid arthritis; multiple sclerosis; inflammatory disorder;
KW atherosclerosis; cardiac injury; infertility; premature aging; AIDS;
KW diabetes; stroke; gene therapy; transgenic; PRO; human.
XX OS Homo sapiens.
XX PN WO200015796-A2.
XX PD 23-MAR-2000.
XX PF 15-SEP-1999; 99WO-US021090.
XX PR 16-SEP-1998; 98WO-US019330.
XX PA (GETH) GENENTECH INC.
XX PI Chen J, Goddard A, Gurney AL, Hillan K, Pennica D, Wood WT;
PI Yuan J;
XX WPI; 2000-271434/23.
XX DR

QY 241 PLACNKGGLWYQIGVWSGVGCGRPNRPGVYTNISHHFEWIKLMAQSGMSQDPSPWLL 300
Db 241 PLACNKGGLWYQIGVWSGVGCGRPNRPGVYTNISHHFEWIKLMAQSGMSQDPSPWLL 300
QY 301 FFPLLWALPLPGPV 314
Db 301 FFPLLWALPLPGPV 314
RESULT 9
AAU02223
ID AAU02223 standard; protein; 314 AA.
XX
AC AAU02223;
XX
DT 29-AUG-2001 (first entry)
XX
DE Human extracellular serine protease TADG-16.
XX
KW Human; extracellular serine protease; tumour antigen derived gene-16;
KW TADG-16; ovarian carcinoma; breast cancer; lung cancer; colon cancer;
KW prostate cancer; HLA type.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..17
FT Protein 18..314 /label= Signal_secretion_sequence
FT Region 76..83 /label= Secreted_TADG-16_protein
FT /note= "Region containing His residue of conserved
FT catalytic triad found in serine proteases"
FT Region 137..141
FT /note= "Region containing Asp residue of conserved
FT catalytic triad found in serine proteases"
FT Region 236..241
FT /note= "Region containing Ser residue of conserved
FT catalytic triad found in serine proteases"
XX
PN WO200127257-A1.
XX
PD 19-APR-2001.
XX
PF 13-OCT-2000; 2000WO-US028558.
XX
PR 14-OCT-1999; 99US-00418557.
XX
PA (UYAR-) UNIV ARKANSAS.
XX
PI O'Brien TJ, Underwood LJ, Shigemasa K;
XX
DR WPI; 2001-273769/28.
DR N-PSDB; AAS01698.
XX
PT New tumor antigen-derived gene-16 protein, useful for diagnosis and
PT treatment of ovarian, breast, lung, colon and prostate cancer.
XX
PS Claim 3; Fig 4; 124pp; English.
XX
CC The present sequence represents a novel human extracellular serine
CC protease, tumour antigen derived gene-16 (TADG-16) protein. TADG-16 is
CC expressed in normal ovaries and testes and in certain ovarian carcinomas.
CC TADG-16 contains the conserved catalytic triad, His-Asp-Ser, and a signal
CC secretion sequence characteristic of the serine protease family. An
CC antisense oligonucleotide having a complementary sequence to the TADG-16
CC nucleic acid is useful for treating various cancers, including ovarian,
CC breast, lung, colon and prostate. The TADG-16 nucleic acid, TADG-16
CC protein and antibodies specific to TADG-16 are useful for the diagnosis
CC of cancer. TADG-16 protein or its fragments are useful for vaccinating an
CC individual against TADG-16. Numerous TADG-16 peptides (AAU02225-AAU02384)
CC are tested for their binding affinity to the 8 haplotypes HLA A0201, HLA
CC A0205, HLA A1, HLA A24, HLA B7, HLA B8, HLA B2702, and HLA B4403

XX SQ Sequence 314 AA;
Query Match 99.7%; Score 1723; DB 4; Length 314;
Best Local Similarity 99.7%; Pred. No. 1.7e-146;
Matches 313; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGARGALLALLARAGLRKPESQEARPLSGPCGRRVITSRIVGGEDAEILGRWPWQGSRLR 60
Db 1 MGARGALLALLARAGLRKPESQEARPLSGPCGRRVITSRIVGGEDAEILGRWPWQGSRLR 60
QY 61 LWDSHVCGVSLLSHRWALTAACHPETYSYDLSDPGMMVQFQGLTSMPSFWSLQAYYTRYF 120
Db 61 LWDSHVCGVSLLSHRWALTAACHPETYSYDLSDPGMMVQFQGLTSMPSFWSLQAYYTRYF 120
QY 121 VSNIIYSPRYLGNSPYDIALVKLSAPVYTKHIQICLOASTFEFENRTDCWVTGWGIK 180
Db 121 VSNIIYSPRYLGNSPYDIALVKLSAPVYTKHIQICLOASTFEFENRTDCWVTGWGIK 180
QY 181 EDEALPSPHTLQEVQVAIINNSMCHLFLKYSFRKDFGDMVCAGNAQGGKACFGDSGG 240
Db 181 EDEALPSPHTLQEVQVAIINNSMCHLFLKYSFRKDFGDMVCAGNAQGGKACFGDSGG 240
QY 241 PLACNKDGLWYQIGVWSGVGCGRPNRPGVYTNISHHFEWIKLMAQSGMSQDPSPWLL 300
Db 241 PLACNKDGLWYQIGVWSGVGCGRPNRPGVYTNISHHFEWIKLMAQSGMSQDPSPWLL 300
QY 301 FFPLLWALPLPGPV 314
Db 301 FFPLLWALPLPGPV 314
RESULT 10
AAE17010
ID AAE17010 standard; protein; 314 AA.
XX
AC AAE17010;
XX
DT 18-APR-2002 (first entry)
XX
DE Human eosinophil serine protease-1 (esp-1) like enzyme #2.
XX
KW Human; eosinophil serine protease-1; esp-1; enzyme; antiinflammatory;
KW antiallergic; osteopathic; cytostatic; dermatological;
KW asthma; airway allergy; chronic obstructive pulmonary disease; COPD;
KW osteoporosis; dermatitis; Paget's disease; therapy.
XX
OS Homo sapiens.
XX
PN WO200198503-A2.
XX
PD 27-DEC-2001.
XX
PF 20-JUN-2001; 2001WO-EP006936.
XX
PR 21-JUN-2000; 2000US-0212844P.
PR 31-OCT-2000; 2000US-0244171P.
PR 30-MAR-2001; 2001US-0279766P.
XX
PA (FARB) BAYER AG.
XX
PI Xiao Y;
XX
DR WPI; 2002-122283/16.
XX
FT Novel purified human eosinophil serine protease 1-like enzyme, useful for
FT identifying modulators of enzyme activity for treating Paget's disease,
FT osteoporosis, airway allergy, asthma.
XX
PS Disclosure; Fig 4; 131pp; English.
XX
CC The invention relates to a purified human eosinophil serine protease-1
CC (esp-1) like enzyme. Esp-1 like enzyme is useful in in-vitro or in-vivo

CC assays to identify test compounds with potential therapeutic or
CC diagnostic value. Esp-1 like enzyme modulator is useful for treating esp-
CC like enzyme dysfunction related diseases condition such as asthma, allergy
CC allergy, chronic obstructive pulmonary disease (COPD) or osteoporosis.
CC Esp-1 like enzyme is also useful in diagnostic assays for detecting
CC diseases and abnormalities or susceptibility to diseases related to
CC presence of mutations in the nucleic acid sequences which encode the
CC enzyme. Pharmaceutical composition comprising esp-1 like enzyme is useful
CC for treating dermatitis, Paget's disease, and preventing degradation of
CC bone implants particularly dental implants. The present sequence is human
CC esp-1 like enzyme
XX
SQ Sequence 314 AA;

Query Match 99.7%; Score 1723; DB 5; Length 314;
Best Local Similarity 99.7%; Pred. No. 1.7e-146;
Matches 313; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGARGALLALLARAGLRKPESQEAAPLSPGCGRRVITSRIVGGEDAEILGRWPWGQSLR 60
Db 1 MGARGALLALLARAGLRKPESQEAAPLSPGCGRRVITSRIVGGEDAEILGRWPWGQSLR 60
Qy 61 LWDSHVCGVSLLSHRWALTAHCEFTYSDLSDPGMMVQFGLTSPFWSLQAYTRYF 120
Db 61 LWDSHVCGVSLLSHRWALTAHCEFTYSDLSDPGMMVQFGLTSPFWSLQAYTRYF 120
Qy 121 VSNLYLSPRYLGNSPYDIALVKLSAPVYTKHIQPICLQASTFEFENRTDCWVTGWGYIK 180
Db 121 VSNLYLSPRYLGNSPYDIALVKLSAPVYTKHIQPICLQASTFEFENRTDCWVTGWGYIK 180
Qy 181 EDEALPSHTLQEVQVAIIINSMCNHILFLKYSPKIDFGDMVCAGNAQGGKACFGDSGG 240
Db 181 EDEALPSHTLQEVQVAIIINSMCNHILFLKYSPKIDFGDMVCAGNAQGGKACFGDSGG 240
Qy 241 PLACNKDGLVYQGVSWGVGCGRPNGVYTNISHHFEMIQKLMAGSGMSQDPDPSPFL 300
Db 241 PLACNKGLVYQGVSWGVGCGRPNGVYTNISHHFEMIQKLMAGSGMSQDPDPSPFL 300
Qy 301 FFPLLWALPLIGPV 314
Db 301 FFPLLWALPLIGPV 314

RESULT 11

ABU71634

ID ABU71634 standard; protein; 314 AA.

AC ABU71634;

XX 16-JUN-2003 (first entry)

XX Human PRO polypeptide #45.

KW Human; PRO; secreted polypeptide; transmembrane polypeptide;
KW pathological disorder; cardiac insufficiency disorder; protein secretion;
KW pancreas; diabetes; gastrointestinal mucosa; mucosal lesion; psoriasis;
KW skin disease; keratinocyte differentiation; epithelial cancer; tumour;
KW lung squamous cell carcinoma; epidermoid carcinoma; vulva; glioma;
KW cytosclastic; cardiac; endocrine; antidiabetic; gastrointestinal;
KW antilucer; dermatological; vulnary.

XX Homo sapiens.

OS US2002146709-A1.

PN 10-OCT-2002.

PD 18-JUL-2001; 2001US-00909088.

XX 17-SEP-1997; 97US-0059113P.

XX 17-SEP-1997; 97US-0059115P.

XX 17-SEP-1997; 97US-0059117P.

XX 17-SEP-1997; 97US-0059119P.

PR 17-SEP-1997; 97US-0059121P.
PR 17-SEP-1997; 97US-0059122P.
PR 17-SEP-1997; 97US-0059184P.
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 18-OCT-1997; 97US-0062125P.
PR 17-OCT-1997; 97US-0062285P.
PR 17-OCT-1997; 97US-0062287P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0062814P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063045P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 24-OCT-1997; 97US-0063127P.
PR 24-OCT-1997; 97US-0063128P.
PR 27-OCT-1997; 97US-0063327P.
PR 27-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063542P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063549P.
PR 28-OCT-1997; 97US-0063550P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063732P.
PR 29-OCT-1997; 97US-0063734P.
PR 29-OCT-1997; 97US-0063735P.
PR 29-OCT-1997; 97US-0063738P.
PR 31-OCT-1997; 97US-0064215P.
PR 31-OCT-1997; 97US-0064103P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 18-NOV-1997; 97US-0065693P.
PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0066772P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 01-DEC-1998; 98WO-US025108.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.

PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00665350.
XX (GETH) GENENTECH INC.
PA Ashkenazi A, Botstein D, Deanovoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Garber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX WPI; 2003-328338/31.
DR N-PSDB; ACA59107.
XX Isolated nucleic acid useful for e.g., treating pathological disorders
PT encodes a secreted or transmembrane protein.
XX Claim 12; Fig 92; 473pp; English.
XX The invention relates to human PRO polypeptides (secreted or
CC transmembrane polypeptides) and the polynucleotides encoding them. The
CC PRO polypeptides and polynucleotides can be used in treating pathological
CC disorders and tumours, in therapeutic treatment of cardiac insufficiency
CC disorders and in therapeutic treatment of disorders involving protein
CC secretion by the pancreas, including diabetes. They can also be used in
CC treating disorders associated with the preservation and maintenance of
CC gastrointestinal mucosa and the repair of acute and chronic mucosal
CC lesions, and skin diseases associated with abnormal keratinocyte
CC differentiation (e.g., psoriasis, epithelial cancers such as lung
CC squamous cell carcinoma, epidermoid carcinoma of the vulva and gliomas).
CC The sequences can be used as molecular markers for protein
CC electrophoresis purposes and can be utilised in protein-protein binding.
CC assays, biochemical screening assays, immunoassays and cell-based assays.
CC This sequence represents a human PRO polypeptide of the invention
XX
SQ Sequence 314 AA;
Query Match 99.7%; Score 1723; DB 6; Length 314;
Best Local Similarity 99.7%; Pred. No. 1.7e-146;
Matches 313; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGARGALLALLARAGLRKPESEAPLSPGCGRRVITSRVGGEDAEILGRNFWQGSRLR 60
Db 1 MGARGALLALLARAGLRKPESEAPLSPGCGRRVITSRVGGEDAEILGRNFWQGSRLR 60
Qy 61 LWDSHVCGVSLSHRWALTAAHCFETYSDDLSPSGMWVQFGLTSMPSFSLQAYTYRYP 120
Db 61 LWDSHVCGVSLSHRWALTAAHCFETYSDDLSPSGMWVQFGLTSMPSFSLQAYTYRYP 120
Qy 121 VSNITLSPRYLGNPYDIALVKLSAPVYTKHIQICLQASTFFENRTDCWVTGWYIK 180
Db 121 VSNITLSPRYLGNPYDIALVKLSAPVYTKHIQICLQASTFFENRTDCWVTGWYIK 180
Qy 181 EDEALPSPHTLQEVQVAILNNMCNHLFLKYSFRKIDFGDMVCAGNAGQGGKACFGDSGG 240
Db 181 EDEALPSPHTLQEVQVAILNNMCNHLFLKYSFRKIDFGDMVCAGNAGQGGKACFGDSGG 240
Qy 241 PLACNKGWLQVIGVSGVCGRPNGPVYTNISHHFEWIKLMAQSGMSQDPSPWPLL 300
Db 241 PLACNKGWLQVIGVSGVCGRPNGPVYTNISHHFEWIKLMAQSGMSQDPSPWPLL 300
Qy 301 FFPLLWALPLLGPV 314
Db 301 FFPLLWALPLLGPV 314
RESULT 12
ID ABU71489
XX ABU71489 standard; protein; 314 AA.
AC ABU71489;
XX
DT 10-JUN-2003 (first entry)

XX Human PRO polypeptide #45.
DE Human; secreted and transmembrane protein; PRO polypeptide; cancer;
XX Alzheimer's disease; ischaemia; cytostatic; nootropic; vasotropic;
KW neuroprotective.
KW Homo sapiens.
OS US2002192659-A1.
XX 19-DEC-2002.
XX 10-JUL-2001; 2001US-00902853.
PF 17-SEP-1997; 97US-0059113P.
XX 17-SEP-1997; 97US-0059115P.
PR 17-SEP-1997; 97US-0059117P.
PR 17-SEP-1997; 97US-0059119P.
PR 17-SEP-1997; 97US-0059121P.
PR 17-SEP-1997; 97US-0059122P.
PR 17-SEP-1997; 97US-0059184P.
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 15-OCT-1997; 97US-0062125P.
PR 17-OCT-1997; 97US-0062285P.
PR 17-OCT-1997; 97US-0062287P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0062814P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063045P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 24-OCT-1997; 97US-0063127P.
PR 24-OCT-1997; 97US-0063128P.
PR 27-OCT-1997; 97US-0063327P.
PR 27-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063542P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063549P.
PR 28-OCT-1997; 97US-0063550P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063732P.
PR 29-OCT-1997; 97US-0063734P.
PR 29-OCT-1997; 97US-0063735P.
PR 29-OCT-1997; 97US-0063738P.
PR 29-OCT-1997; 97US-0064215P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 18-NOV-1997; 97US-0065693P.
PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0066772P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 01-DEC-1998; 98WO-US025108.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.

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PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028564.
PR 16-DEC-1999; 99WO-US028565.
PR 20-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00665350.
XX
XX (GETH ) GENENTECH INC.
FA
XX Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX
XX WPI; 2003-361832/34.
DR N-PSDB; ACA58504.
XX
XX New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO245 or
PT PRO1868, useful in molecular biology, chromosome and gene mapping, in
FT generating antisense RNA and DNA, and in gene therapy.
XX
XX Claim 12; Fig 92; 474pp; English.
XX
XX The present invention relates to the isolation of novel human secreted
CC and transmembrane proteins (PRO polypeptides), and the polynucleotide
CC sequences encoding them. The polynucleotide sequences are useful in
CC molecular biology, as hybridisation probes, in chromosome and gene
CC mapping, in generating antisense RNA and DNA, and in gene therapy. The
CC polynucleotide sequences may also be used in preparing PRO polypeptides
CC by recombinant techniques, and in generating either transgenic animals or
CC knock-out animals which, in turn, are useful in the development and
CC screening of therapeutically useful reagents. The PRO polypeptides or
CC their antibodies are useful in preparing a medicament for treating a
CC condition responsive to the polypeptide or antibody, such as cancer,
CC Alzheimer's disease or ischaemia, and in various diagnostic assays.
CC ABU71445-ABU71505 represent human PRO polypeptides of the invention
XX
XX Sequence 314 AA;
SQ
Query Match 99.7%; Score 1723; DB 6; Length 314;
Best Local Similarity 99.7%; Pred. No. 1.7e-146;
Matches 313; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGARGALLALLARAGLRKPESQEAAPLPGCGRRVITSRVGGEDAEILGRWPQGSRLR 60
Db 1 MGARGALLALLARAGLRKPESQEAAPLPGCGRRVITSRVGGEDAEILGRWPQGSRLR 60
Qy 61 LWDSHVCGVSLLSHRWALTAAHCFTETYSDDLSDPSGMMVQFCOLTSMPSEFSLQAYTRYF 120
Db 61 LWDSHVCGVSLLSHRWALTAAHCFTETYSDDLSDPSGMMVQFCOLTSMPSEFSLQAYTRYF 120
Qy 121 VSNLYLSPRYLGNSPYDIALVKLSAPVYTKHQIPICLQASTFFENRTDCWVTGWCYIK 180
Db 121 VSNLYLSPRYLGNSPYDIALVKLSAPVYTKHQIPICLQASTFFENRTDCWVTGWCYIK 180
Qy 181 EDEALPSHTLQEVQVAIINNMCNHLFLKYSFRKDFGDMVCAGNAQGGKACFGDSGG 240
..
```

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Db 181 EDEALPSHTLQEVQVAIINNMCNHLFLKYSFRKDFGDMVCAGNAQGGKACFGDSGG 240
Qy 241 PLACNKDGLWYQIGVSVGWGCGRPNRPGVYTNISHHFEWIOKLMAQSGMSQDPSPWPLL 300
Db 241 PLACNKDGLWYQIGVSVGWGCGRPNRPGVYTNISHHFEWIOKLMAQSGMSQDPSPWPLL 300
Qy 301 FFPELLWALPLLGPV 314
Db 301 FFPELLWALPLLGPV 314
RESULT 13
ABU71935
ID ABU71935 standard; protein; 314 AA.
XX
XX AC ABU71935;
XX
XX 12-JUN-2003 (first entry)
XX
XX Human secreted/transmembrane protein PRO303.
XX
XX Human; secreted protein; transmembrane protein; PRO; gene therapy;
XX chromosome identification; chromosome marker.
XX
XX Homo sapiens.
XX
XX US2003003530-A1.
XX
XX 02-JAN-2003.
XX
XX 11-JUL-2001; 2001US-00904011.
XX
XX 17-SEP-1997; 97US-0059113P.
XX 17-SEP-1997; 97US-0059115P.
XX 17-SEP-1997; 97US-0059117P.
XX 17-SEP-1997; 97US-0059119P.
XX 17-SEP-1997; 97US-0059121P.
XX 17-SEP-1997; 97US-0059122P.
XX 17-SEP-1997; 97US-0059184P.
XX 18-SEP-1997; 97US-0059263P.
XX 18-SEP-1997; 97US-0059266P.
XX 15-OCT-1997; 97US-0062125P.
XX 17-OCT-1997; 97US-0062285P.
XX 17-OCT-1997; 97US-0062287P.
XX 21-OCT-1997; 97US-0063486P.
XX 24-OCT-1997; 97US-0062814P.
XX 24-OCT-1997; 97US-0062816P.
XX 24-OCT-1997; 97US-0063045P.
XX 24-OCT-1997; 97US-0063120P.
XX 24-OCT-1997; 97US-0063121P.
XX 24-OCT-1997; 97US-0063127P.
XX 24-OCT-1997; 97US-0063128P.
XX 27-OCT-1997; 97US-0063327P.
XX 27-OCT-1997; 97US-0063329P.
XX 28-OCT-1997; 97US-0063541P.
XX 28-OCT-1997; 97US-0063542P.
XX 28-OCT-1997; 97US-0063544P.
XX 28-OCT-1997; 97US-0063549P.
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XX 28-OCT-1997; 97US-0063564P.
XX 28-OCT-1997; 97US-0063435P.
XX 29-OCT-1997; 97US-0063704P.
XX 29-OCT-1997; 97US-0063732P.
XX 29-OCT-1997; 97US-0063734P.
XX 29-OCT-1997; 97US-0063735P.
XX 29-OCT-1997; 97US-0063738P.
XX 29-OCT-1997; 97US-0064215P.
XX 31-OCT-1997; 97US-0063870P.
XX 31-OCT-1997; 97US-0064103P.
XX 03-NOV-1997; 97US-0064248P.
XX 07-NOV-1997; 97US-0064809P.
XX 12-NOV-1997; 97US-0065186P.
XX 17-NOV-1997; 97US-0065846P.
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PR 18-NOV-1997; 97US-0065693P.
 PR 21-NOV-1997; 97US-0066120P.
 PR 21-NOV-1997; 97US-0066364P.
 PR 24-NOV-1997; 97US-0066453P.
 PR 24-NOV-1997; 97US-0066466P.
 PR 24-NOV-1997; 97US-0066511P.
 PR 24-NOV-1997; 97US-0066770P.
 PR 24-NOV-1997; 97US-0066772P.
 PR 10-SEP-1998; 98WO-US018824.
 PR 14-SEP-1998; 98WO-US019177.
 PR 16-SEP-1998; 98WO-US019330.
 PR 17-SEP-1998; 98WO-US019437.
 PR 01-DEC-1998; 98WO-US025108.
 PR 08-SEP-1998; 98WO-US020594.
 PR 13-SEP-1999; 99WO-US020944.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 05-OCT-1999; 99WO-US023089.
 PR 29-NOV-1999; 99WO-US028214.
 PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028301.
 PR 02-DEC-1999; 99WO-US028564.
 PR 02-DEC-1999; 99WO-US028565.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 20-DEC-1999; 99WO-US030999.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 18-SEP-2000; 2000US-00665350.
 XX
 XX (GETH) GENENTECH INC.
 XX
 PI Ashkenazi A, Botstein D, Desnovers L, Eaton DL, Ferrara N;
 PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen WE, Goddard A;
 PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
 PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
 PI Williams PW, Wood WI;
 XX
 DR WPI; 2003-329602/31.
 DR N-PSDB; ACA60211.
 XX
 PT New transmembrane polypeptides and nucleic acids encoding the
 PT polypeptides, useful in gene therapy, in chromosome identification, as
 PT chromosome markers, in generating probes and in tissue typing.
 XX
 XX Claim 12; Fig 92; 484pp; English.
 XX
 XX The invention relates to an isolated nucleic acid with at least 80%
 CC nucleic acid sequence identity to a nucleotide sequence encoding one of
 CC 61 secreted/transmembrane polypeptides, or PRO polypeptides or encoding a
 CC PRO protein extracellular domain. Also included are a vector comprising
 CC the PRO nucleic acid, a host cell comprising the vector, producing a PRO
 CC polypeptide (by culturing the host cell for the expression of the PRO
 CC polypeptide, and recovering the PRO polypeptide from the cell culture),
 CC an isolated PRO polypeptide (having at least 80% sequence identity to:
 CC a) an amino acid sequence selected from the 61 PRO proteins; (b) an amino
 CC acid sequence encoded by a nucleic acid molecule deposited with an ATCC
 CC number (detailed in the specification); or (c) an extracellular domain of
 CC a PRO polypeptide or to a PRO polypeptide lacking its associated signal
 CC peptide), a chimeric molecule comprising a PRO polypeptide of fused to a
 CC heterologous amino acid sequence, an anti-PRO antibody, detecting a
 CC PRO245 or PRO1868 in a sample suspected of containing the polypeptide,
 CC linking a bioactive molecule to a cell expressing a PRO245 or PRO1868 and
 CC modulating at least one biological activity of a cell expressing a PRO245

CC or PRO1868. Nucleic acids which encode PRO can be used to generate either
 CC transgenic animals or knock-out animals which may be used in the
 CC development and screening of therapeutically useful reagents. The nucleic
 CC acids may also be used in gene therapy, in chromosome identification, as
 CC chromosome markers, or in generating probes. The PRO polypeptides are
 CC useful as molecular markers for protein electrophoresis, and the isolated
 CC nucleic acids may be used for recombinantly expressing those markers. The
 CC PRO polypeptides and nucleic acids may also be used in tissue typing.
 CC Anti-PRO antibodies are useful in diagnostic assays for PRO, and in
 CC affinity purification of PRO from recombinant cell culture or natural
 CC sources. The present sequence represents a PRO protein
 XX
 XX Sequence 314 AA;

Query Match 99.7%; Score 1723; DB 6; Length 314;
 Best Local Similarity 99.7%; Pred. No. 1.7e-146;
 Matches 313; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGARGALLALLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEAEELGRWPQGSRLR 60
 DB 1 MGARGALLALLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEAEELGRWPQGSRLR 60
 QY 61 LWDSHVCGVSLLSHRWALTAHCFETYSDLSDPGSMVQFGLTSMPSFWSLQAYTRYF 120
 DB 61 LWDSHVCGVSLLSHRWALTAHCFETYSDLSDPGSMVQFGLTSMPSFWSLQAYTRYF 120
 QY 121 VSNITLSPRYLGNSPYDIALVKLSAPVYTKHQIPICLQASTFPEFNRDTCWVTGWGIK 180
 DB 121 VSNITLSPRYLGNSPYDIALVKLSAPVYTKHQIPICLQASTFPEFNRDTCWVTGWGIK 180
 QY 181 EDEALPSPHTLOEVQVVAIINNSMCNHLFLKYSFKDIFGDMVCAGNAQGGKACFGDSGG 240
 DB 181 EDEALPSPHTLOEVQVVAIINNSMCNHLFLKYSFKDIFGDMVCAGNAQGGKACFGDSGG 240
 QY 241 PLACNKDGLWYQIGVSWGVGCGRPNRPVYVYTNISHHFEWIKLMAQSGMSQPPSPWLL 300
 DB 241 PLACNKDGLWYQIGVSWGVGCGRPNRPVYVYTNISHHFEWIKLMAQSGMSQPPSPWLL 300
 QY 301 FFPILLWALPLIGPV 314
 DB 301 FFPILLWALPLIGPV 314

RESULT 14
 ABO01818
 ID ABO01818 standard; protein; 314 AA.
 XX
 AC ABO01818;
 XX
 DT 07-AUG-2003 (first entry)
 XX
 DE Novel human secreted and transmembrane protein PRO303.
 XX
 KW Human; secreted and transmembrane protein; PRO; pharmaceutical;
 KW diagnostic; biosensor; bioreactor; Parkinson's disease;
 KW Alzheimer's disease; inflammation; nephritis; wound healing;
 KW nerve repair; collateral blood vessel formation; cancer;
 KW colorectal cancer; haemorrhage; rheumatoid arthritis; diabetes;
 KW cirrhosis; fibrosis; restenosis; dermal fibrotic condition; keloid;
 KW scarring; ischaemia; stroke; hypertension; heart attack; atherosclerosis;
 KW infertility; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN US2002197671-A1.
 XX
 XX 26-DEC-2002.
 PD
 XX 17-JUL-2001; 2001US-00907824.
 PF
 XX 17-SEP-1997; 97US-0059113P.
 PR 17-SEP-1997; 97US-0059115P.
 PR 17-SEP-1997; 97US-0059117P.

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PR 17-SEP-1997; 97US-0059119P.
PR 17-SEP-1997; 97US-0059121P.
PR 17-SEP-1997; 97US-0059122P.
PR 17-SEP-1997; 97US-0059184P.
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 15-OCT-1997; 97US-0062125P.
PR 17-OCT-1997; 97US-0062285P.
PR 17-OCT-1997; 97US-0062287P.
PR 21-OCT-1997; 97US-0063486P.
PR 21-OCT-1997; 97US-0062814P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063045P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 24-OCT-1997; 97US-0063137P.
PR 24-OCT-1997; 97US-0063138P.
PR 27-OCT-1997; 97US-0063327P.
PR 27-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063542P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063549P.
PR 28-OCT-1997; 97US-0063550P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063732P.
PR 29-OCT-1997; 97US-0063734P.
PR 29-OCT-1997; 97US-0063735P.
PR 29-OCT-1997; 97US-0063738P.
PR 29-OCT-1997; 97US-0064215P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 18-NOV-1997; 97US-0065693P.
PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0066772P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 01-DEC-1998; 98WO-US025108.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 30-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.

PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00665350.
XX
XX (GETH ) GENENTECH INC.
XX Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N,
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX WPI; 2003-370793/35.
DR N-PSDB; ACD07611.
XX
XX New genes and secreted and transmembrane polypeptides (e.g. PRO245 or
PT PRO335), useful for treating or diagnosing e.g. Alzheimer's disease,
PT cancers, hemorrhage, rheumatoid arthritis, diabetes, cirrhosis, ischemia
PT or strokes.
XX
XX Claim 12; Fig 92; 482pp; English.
XX
XX The invention describes a new isolated nucleic acid molecule comprising
CC the full length coding sequence of the DNA deposited with the American
CC Type Culture Collection (e.g. ATCC Deposit No. 209258), or a sequence
CC with at least 80% identity to a DNA encoding a PRO polypeptide comprising
CC any of 61 sequences having 164-1119 amino acids fully defined in the
CC specification. The PRO polypeptides or polynucleotides are useful as
CC pharmaceuticals, diagnostics, biosensors or bioreactors. These are
CC particularly useful for detecting or treating e.g. Parkinson's disease,
CC Alzheimer's disease, inflammations, nephritis, wound healing, nerve
CC repair, collateral blood vessel formation, cancers (e.g. colorectal
CC cancer), haemorrhage (or reduce risk for haemorrhage), rheumatoid
CC arthritis, diabetes, cirrhosis of the liver, fibrosis of the lungs,
CC restenosis, dermal fibrotic conditions (e.g. keloids or scarring), or
CC ischaemia, strokes, hypertension, heart attacks, atherosclerosis, or
CC infertility in mammals (e.g. humans, dogs, cats, cattle, horses, sheep,
CC pigs, goats, or rabbits). The PRO polypeptides are useful as targets for
CC therapeutic intervention in these diseases, and diagnostic determination
CC of the presence of these diseases. The PRO polypeptides are also useful
CC as molecular weight markers, or for chromosome identification. The PRO
CC genes are useful as hybridisation probes, or for screening libraries of
CC human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene
CC therapy, particularly for replacing a defective gene. This is the amino
CC acid sequence of a novel human secreted and transmembrane PRO polypeptide
XX
XX Sequence 314 AA;
SQ
Query Match 99.7%; Score 1723; DB 6; Length 314;
Best Local Similarity 99.7%; Pred. No. 1.7e-146;
Matches 313; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGARGALLALLARAGLRKPESQEAAPLSGPGRRVITSRIVGGDAELGRPWQGSRLR 60
DB 1 MGARGALLALLARAGLRKPESQEAAPLSGPGRRVITSRIVGGDAELGRPWQGSRLR 60
QY 61 LWDSHVCGVSLSHRWALTAHCFETYSDLSDPGMMVQFQGLTSPFWSLQAYTRYF 120
DB 61 LWDSHVCGVSLSHRWALTAHCFETYSDLSDPGMMVQFQGLTSPFWSLQAYTRYF 120
QY 121 VSNILSPRYLGNSPYDIALVKLSAPVYTKHIQPICLQASTFEFENRDCWVTGWGIK 180
DB 121 VSNILSPRYLGNSPYDIALVKLSAPVYTKHIQPICLQASTFEFENRDCWVTGWGIK 180
QY 181 EDEALSPHTLQEVQVAIIINNSCNHLFLKYSFRKDI FGMVCAAGKACFDGSG 240
DB 181 EDEALSPHTLQEVQVAIIINNSCNHLFLKYSFRKDI FGMVCAAGKACFDGSG 240
QY 241 PLACNKDGLWYQIGVSVGWGCGRPNRPGVYTNISHHFEWIOKLMAQSGMSQDPSPWLL 300
DB 241 PLACNKDGLWYQIGVSVGWGCGRPNRPGVYTNISHHFEWIOKLMAQSGMSQDPSPWLL 300
QY 301 FPLLLWALPLLGPV 314
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Db 301 PFPLLWALPLGPFV 314
 |||||
 RESULT 15
 ABUS4391
 ID ABUS4391 standard; protein; 314 AA.
 XX
 AC ABUS4391;
 XX
 DT 10-MAR-2003 (first entry)
 XX
 DE Human secreted/transmembrane protein PRO303.
 XX
 KW Human; PRO; secreted protein; transmembrane protein; enterocolitis;
 KW gastrointestinal ulceration; skin disease;
 KW abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
 KW squamous cell carcinoma; Alzheimer's disease; Parkinson's disease;
 KW amyotrophic lateral sclerosis; inflammatory disease;
 KW rheumatoid arthritis; asthma; multiple sclerosis; organ failure;
 KW atherosclerosis; cardiac injury; infertility; birth defect;
 KW premature aging; AIDS; acquired immunodeficiency syndrome; cancer;
 KW diabetic complication; wound repair.
 XX
 OS Homo sapiens.
 XX
 PN US2002132240-A1.
 XX
 PD 19-SEP-2002.
 XX
 PF 18-JUL-2001; 2001US-00909320.
 XX
 PR 17-SEP-1997; 97US-0059113P.
 PR 17-SEP-1997; 97US-0059113P.
 PR 17-SEP-1997; 97US-0059117P.
 PR 17-SEP-1997; 97US-0059117P.
 PR 17-SEP-1997; 97US-0059121P.
 PR 17-SEP-1997; 97US-0059121P.
 PR 17-SEP-1997; 97US-0059122P.
 PR 17-SEP-1997; 97US-0059184P.
 PR 18-SEP-1997; 97US-0059263P.
 PR 18-SEP-1997; 97US-0059266P.
 PR 15-OCT-1997; 97US-0062125P.
 PR 17-OCT-1997; 97US-0062285P.
 PR 17-OCT-1997; 97US-0062287P.
 PR 21-OCT-1997; 97US-0062348P.
 PR 24-OCT-1997; 97US-0062381P.
 PR 24-OCT-1997; 97US-0062816P.
 PR 24-OCT-1997; 97US-0063045P.
 PR 24-OCT-1997; 97US-0063120P.
 PR 24-OCT-1997; 97US-0063121P.
 PR 24-OCT-1997; 97US-0063127P.
 PR 24-OCT-1997; 97US-0063128P.
 PR 27-OCT-1997; 97US-0063327P.
 PR 27-OCT-1997; 97US-0063329P.
 PR 28-OCT-1997; 97US-0063541P.
 PR 28-OCT-1997; 97US-0063542P.
 PR 28-OCT-1997; 97US-0063544P.
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 PR 28-OCT-1997; 97US-0063550P.
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 PR 29-OCT-1997; 97US-0063732P.
 PR 29-OCT-1997; 97US-0063734P.
 PR 29-OCT-1997; 97US-0063735P.
 PR 29-OCT-1997; 97US-0063738P.
 PR 29-OCT-1997; 97US-0064215P.
 PR 31-OCT-1997; 97US-0063870P.
 PR 31-OCT-1997; 97US-0064103P.
 PR 31-OCT-1997; 97US-0064248P.
 PR 07-NOV-1997; 97US-0064809P.
 PR 12-NOV-1997; 97US-0065186P.
 PR 17-NOV-1997; 97US-0065846P.

18-NOV-1997; 97US-0065693P.
 21-NOV-1997; 97US-0066120P.
 21-NOV-1997; 97US-0066364P.
 24-NOV-1997; 97US-0066453P.
 24-NOV-1997; 97US-0066466P.
 24-NOV-1997; 97US-0066511P.
 24-NOV-1997; 97US-0066770P.
 24-NOV-1997; 97US-0066772P.
 10-SEP-1998; 98WO-US018824.
 14-SEP-1998; 98WO-US019177.
 16-SEP-1998; 98WO-US019330.
 17-SEP-1998; 98WO-US019437.
 01-DEC-1998; 98WO-US025108.
 08-SEP-1999; 98WO-US020594.
 13-SEP-1999; 99WO-US020944.
 15-SEP-1999; 99WO-US021090.
 15-SEP-1999; 99WO-US021547.
 05-OCT-1999; 99WO-US023089.
 29-NOV-1999; 99WO-US028214.
 30-NOV-1999; 99WO-US028313.
 01-DEC-1999; 99WO-US028301.
 02-DEC-1999; 99WO-US028564.
 02-DEC-1999; 99WO-US028565.
 16-DEC-1999; 99WO-US030095.
 20-DEC-1999; 99WO-US030911.
 20-DEC-1999; 99WO-US030999.
 06-JAN-2000; 2000WO-US000219.
 11-FEB-2000; 2000WO-US003565.
 22-FEB-2000; 2000WO-US004414.
 24-FEB-2000; 2000WO-US005004.
 02-MAR-2000; 2000WO-US005841.
 20-MAR-2000; 2000WO-US007377.
 20-MAR-2000; 2000WO-US008439.
 22-MAY-2000; 2000WO-US014042.
 02-JUN-2000; 2000WO-US015264.
 28-JUL-2000; 2000WO-US020710.
 24-AUG-2000; 2000WO-US023328.
 18-SEP-2000; 2000US-00665350.

(GETH) GENENTECH INC.
 Ashkenazi A, Botstein D, Deenoyers L, Eaton DL, Ferrara N;
 Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
 Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
 Williams PM, Wood WI;
 WPI; 2003-147434/14.
 N-FSDB; AEX71659.

New PRO polypeptides and nucleic acid molecules, useful in diagnosing or treating inflammatory diseases, organ failure, atherosclerosis, cardiac injury, infertility, cancer, AIDS, Alzheimer's disease or Parkinson's disease.

Claim 12; Fig 92; 473pp; English.

The invention relates to an isolated PRO polypeptide having at least 80% amino acid sequence identity to: (a) any one of 61 fully defined amino acid sequences given in the specification (appearing as ABUS4347-ABUS4407); (b) an amino acid sequence encoded by the nucleotide sequence deposited under American Type Culture Collection (accession numbers listed in the specification); (c) any one of the PRO sequences which lacks its associated signal peptide; (d) an extracellular domain of the PRO polypeptide with its associated signal peptide; or (e) an extracellular domain of the PRO polypeptide which lacks its associated signal peptide. Also include are the nucleic acids encoding the PRO polypeptides, vectors, host cells and anti-PRO antibodies. The PRO polypeptides and nucleic acids are useful in diagnosing or treating enterocolitis, gastrointestinal ulceration, skin diseases associated with abnormal keratinocyte differentiation, e.g. psoriasis or epithelial cancers such as squamous cell carcinoma, Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis, inflammatory diseases, e.g.

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CC rheumatoid arthritis, asthma or multiple sclerosis, organ failure,  
CC atherosclerosis, cardiac injury, infertility, birth defects, premature  
CC aging, AIDS, cancer, diabetic complications, or mutations in general. The  
CC polypeptides are also useful for wound repair and associated therapies  
CC concerned with re-growth of tissue. The nucleotide sequences may be used  
CC as hybridisation probes in chromosome and gene mapping, or in generating  
CC antisense RNA and DNA. PRO nucleic acids are also useful in preparing PRO  
CC polypeptides, in assays to identify other proteins or molecules involved  
CC in binding reaction, to generate transgenic animals or knockout animals,  
CC which in turn are useful in the development and screening of  
CC therapeutically useful reagents, for chromosome identification, and  
CC tissue typing. The PRO polypeptides and nucleic acid molecules are also  
CC useful in gene therapy, and as molecular weight markers for protein  
CC electrophoresis purposes. The anti-PRO antibodies may be used in  
CC diagnostic assays for PRO, or for the affinity purification of PRO from  
CC recombinant cell culture or natural sources. The present sequence  
CC represents a PRO polypeptide  
XX  
SQ Sequence 314 AA;  
Query Match 99.7%; Score 1723; DB 6; Length 314;  
Best Local Similarity 99.7%; Pred. No. 1.7e-146;  
Matches 313; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MGARGALLALLARAGLRKPESQEAAPLSGPGCRRVITSRIVGGEDAELGRWPWGSLR 60  
Db 1 MGARGALLALLARAGLRKPESQEAAPLSGPGCRRVITSRIVGGEDAELGRWPWGSLR 60  
Qy 61 LWDSHVCGVSLLSHRWALTAHCFETYSDLSDPGMMVQFQLTSMPSFWSLQAYYTRYF 120  
Db 61 LWDSHVCGVSLLSHRWALTAHCFETYSDLSDPGMMVQFQLTSMPSFWSLQAYYTRYF 120  
Qy 121 VSNLYLSPRYLGNPYDIALVKLSAPVTTYTKHIQPICLQASTFEFENRTDCWVTGWGYIK 180  
Db 121 VSNLYLSPRYLGNPYDIALVKLSAPVTTYTKHIQPICLQASTFEFENRTDCWVTGWGYIK 180  
Qy 181 EDEALPSPHTLQEVQVAIIINNSMCNHLFLKYSFRKIDFGDMVCAGNAQGGKDACFGDSGG 240  
Db 181 EDEALPSPHTLQEVQVAIIINNSMCNHLFLKYSFRKIDFGDMVCAGNAQGGKDACFGDSGG 240  
Qy 241 PLACNKDGLWYQIGVWSGVCGRPNRPGVYTNISHHFEWIKLMAQSGMSQDPDPSPWLL 300  
Db 241 PLACNKDGLWYQIGVWSGVCGRPNRPGVYTNISHHFEWIKLMAQSGMSQDPDPSPWLL 300  
Qy 301 FFLLWALPLGPV 314  
Db 301 FFLLWALPLGPV 314
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Search completed: February 27, 2005, 20:22:32
Job time : 118.374 secs

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4	4	870.4	79.1	884	1	AL555870	AL555870
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23	472.4	42.9	628	4	BG177347	BG177347	
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QY 61 GGCTGGACTCAGGAAGCCGGAGTCGCGAGGAGCGCGCGTATATCAGGACCATCGCGCCG 120
D 63 GGCTGGACTCAGGAAGCCGGAGTCGCGAGGAGCGCGCGTATATCAGGACCATCGCGCCG 122
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D 123 ACGGGTCATCAGCTCGCGCATCGTGGGTGGAGAGGACGCCGAATCGCGGGTGTGGCGGTG 182
QY 181 GCAGGGAGCTGGCGCTGTGGATTCACAGTATGCGGAGTGGAGTGGAGTGGAGTGGAGTGG 240
D 183 GCAGGGAGCTGGCGCTGTGGATTCACAGTATGCGGAGTGGAGTGGAGTGGAGTGGAGTGG 242
QY 241 CTGGGCACTCAGCGCGCGCACTGCTTTGAAACCTATAGTACCTTAGTATGATCCCTCCGG 300
D 243 CTGGGCACTCAGCGCGCGCACTGCTTTGAAACCTATAGTACCTTAGTATGATCCCTCCGG 302
QY 301 GTGGATGGTCCAGTTGGCCAGCTGACTTCCATGCCATCTTCTGGAGCCTGCGAGGCTTA 360
D 303 GTGGATGGTCCAGTTGGCCAGCTGACTTCCATGCCATCTTCTGGAGCCTGCGAGGCTTA 362
QY 361 CTACACCGTTACTTCTGATCGAATATCTATCTGAGCGCTCGTACCTGGGGAATTCACC 420
D 363 CTACACCGTTACTTCTGATCGAATATCTATCTGAGCGCTCGTACCTGGGGAATTCACC 422
QY 421 CTATGACATTCGCTTGTGAGGCTGTCTGACACCTGTCACTTACACTAAACACATCCAGCC 480
D 423 CTATGACATTCGCTTGTGAGGCTGTCTGACACCTGTCACTTACACTAAACACATCCAGCC 482
QY 481 CATCTGTCTCAGGCTCCCAATTTGAGTTGAGAACCGGACAGACTGCTGGGTGACTGG 540
D 483 CATCTGTCTCAGGCTCCCAATTTGAGTTGAGAACCGGACAGACTGCTGGGTGACTGG 542
QY 541 CTGGGGGTACATCAAGAGGATGAGGCACTGCCATCTCCCCACACCTCCAGGAGTTCA 600
D 543 CTGGGGGTACATCAAGAGGATGAGGCACTGCCATCTCCCCACACCTCCAGGAGTTCA 602
QY 601 GGTCCCATCATAAACAACTTATGTGCAACCACTCTTCTCAAGTACAGTTTCCGCAA 660
D 603 GGTCCCATCATAAACAACTTATGTGCAACCACTCTTCTCAAGTACAGTTTCCGCAA 662
QY 661 GGACATCTTTGGAGACATGTTGTGTGGCAATGCCCCAAGCGCGGGAAGATGCTGCT 720
D 663 GGACATCTTTGGAGACATGTTGTGTGGCAATGCCCCAAGCGCGGGAAGATGCTGCT 722
QY 721 CGGTGACTCAGGTGACCTTGGCTGTAAACGATGAGTGTGATCAGATTGAGT 780
D 723 CGGTGACTCAGGTGACCTTGGCTGTAAACGATGAGTGTGATCAGATTGAGT 782
QY 781 CGTGAGCTGGGGAGTGGGCTGTGTGCGGCCCAATCGGCCCGGCTGTACACCAATATCAG 840
D 783 CGTGAGCTGGGGAGTGGGCTGTGTGCGGCCCAATCGGCCCGGCTGTACACCAATATCAG 842
QY 841 CCACCACTTTGAGTGGATCCAGAGCTGATGCGCCACAGAGTGGCATGTCCAGCCAGACCC 900
D 843 CCACCACTTTGAGTGGATCCAGAGCTGATGCGCCACAGAGTGGCATGTCCAGCCAGACCC 902
QY 901 CTCCTGCGCGTACTCTTTTCCCTTCTCTGCGGCTCTCCACTCTCGGGCGCGGCTG 960
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QY 961 AGCCTACTGAGCCCATGAGCCTTGGGGCCACTGCCAAGTCAGGCCCTGTCTTCTCTG 1020
D 963 AGCCTACTGAGCCCATGAGCCTTGGGGCCACTGCCAAGTCAGGCCCTGTCTTCTCTG 1022
QY 1021 TCTTGTGTTGTAATAACATTCAGTTGATGCTTGAGGCGATTTTCAAAA 1075
D 1023 TCTTGTGTTGTAATAACATTCAGTTGATGCTTGAGGCGATTTTCAAAA 1077
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RESULT 2
CR605277 1014 bp mRNA linear HTC 21-JUL-2004
LOCUS
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DEFINITION full-length cDNA clone CS0DK002YM07 of HeLa cells Cot 25-normalized of Homo sapiens (human).

ACCESSION CR605277

VERSION CR605277.1 GI:50486084

KEYWORDS HTC; CNSLIT_CDNA.

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE 1. (bases 1 to 1014) Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished JOURNAL

REMARK Contact : Peng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ invitrogen Corporation 1600 Faraday Avenue

REFERENCE 2. (bases 1 to 1014) Genoscope. Direct Submission Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

FEATURES

Location/Qualifiers

1..1014

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DK002YM07"

/tissue_type="HeLa cells Cot 25-normalized"

/plasmid="pCMVSPORT_6"

ORIGIN

Query Match 92.0%; Score 1012.4; DB 3; Length 1014;

Best Local Similarity 99.9%; Pred. No. 1.3e-243;

Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CGGAGAGGAGGCGCATGCGCGCGCGCGCGCGCGCGCTGCTGCTGGCTGGCTGG 62

D 1 CGGAGAGGAGGCGCATGCGCGCGCGCGCGCGCGCGCTGCTGCTGGCTGGCTGG 60

QY 63 CTGAGCTCAGAGAGCGGAGTTCGAGAGCGCGCGCGCTTATCAGGACCATGCGGCGC 122

D 61 CTGAGCTCAGAGAGCGGAGTTCGAGAGCGCGCGCGCTTATCAGGACCATGCGGCGC 120

QY 123 GGTTCATCAGCTCGCGCATCGTGGGTGGAGAGACCGCGAACTCGGCGCTTGGCGCTGG 182

D 121 GGTTCATCAGCTCGCGCATCGTGGGTGGAGAGACCGCGAACTCGGCGCTTGGCGCTGG 180

QY 183 AGGGAGCGCTGCGCGCTGTGGGATTCACAGTATCGGAGTGGAGCTGCTCAGCACCGCT 242

D 181 AGGGAGCGCTGCGCGCTGTGGGATTCACAGTATCGGAGTGGAGCTGCTCAGCACCGCT 240

QY 243 GGCACCTCAGCGCGCGCACTGCTTTGAAACCTATAGTACCTTAGTATGATCCCTCCGGGT 302

D 241 GGCACCTCAGCGCGCGCACTGCTTTGAAACCTATAGTACCTTAGTATGATCCCTCCGGGT 300

QY 303 GGTATGTTCCAGTTGGCGAGCTGACTTCCATGCCATCTTCTGAGAGCTTGAAGCTTACT 362

D 301 GGTATGTTCCAGTTGGCGAGCTGACTTCCATGCCATCTTCTGAGAGCTTGAAGCTTACT 360

QY 363 ACACCGGTTACTTCTGATTCGAATATCTATCTGAGCGCTCGCTACCTGGGGAATTCACCT 422

D 361 ACACCGGTTACTTCTGATTCGAATATCTATCTGAGCGCTCGCTACCTGGGGAATTCACCT 420

QY 423 ATGACATTGCTGGTGAAGCTGTCTGCACCTGTCTACCTTACACTTAAACACATCCAGCCCA 482

D 421 ATGACATTGCTGGTGAAGCTGTCTGCACCTGTCTACCTTACACTTAAACACATCCAGCCCA 480

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QY 483 TCTCTCTCCAGGCTCCACATTTGAGTTGAGAACCGGACAGACTGCTGGTGACTGGCT 542
Db 481 TCTGTCTCCAGGCTCCACATTTGAGTTGAGAACCGGACAGACTGCTGGTGACTGGCT 540
QY 543 GGGGGTACATCAAGAGAGATGAGGACACTGCCATCTCCGCCACACCTCCAGGAAGTTCAGG 602
Db 541 GGGGGTACATCAAGAGAGATGAGGACACTGCCATCTCCGCCACACCTCCAGGAAGTTCAGG 600
QY 603 TCGCCATCATAAACAACCTCTATGTGCAACACCTCTTCTCTCAAGTACAGTTTCGGCAAGG 662
Db 601 TCGCCATCATAAACAACCTCTATGTGCAACACCTCTTCTCTCAAGTACAGTTTCGGCAAGG 660
QY 663 ACATCTTTGGAGACATGGTTTGTCTGTCATGCGCATGCGGCGGCAAGGATGCTGCTTCG 722
Db 661 ACATCTTTGGAGACATGGTTTGTCTGTCATGCGCATGCGGCGGCAAGGATGCTGCTTCG 720
QY 723 GTGACTCAGGTGGACCTTGGCTGTGTAACAGGATGGAAGTGTGATATCAGATTGGAGTCG 782
Db 721 GTGACTCAGGTGGACCTTGGCTGTGTAACAGGATGGAAGTGTGATATCAGATTGGAGTCG 780
QY 783 TGAGCTGGGGAGTGGGCTGTGGTCCGCCCAATCGGCCGGGTGTCTACACCAATATCAGCC 842
Db 781 TGAGCTGGGGAGTGGGCTGTGGTCCGCCCAATCGGCCGGGTGTCTACACCAATATCAGCC 840
QY 843 ACCACTTTGAGTGATCAGAAAGCTGATGGCCAGAGTGGATGTCAGGCGCAGACCCCT 902
Db 841 ACCACTTTGAGTGATCAGAAAGCTGATGGCCAGAGTGGATGTCAGGCGCAGACCCCT 900
QY 903 CTTGGCCGCTACTCTTTTCCCTCTCTCTGGGCTCTCCCACTCTGGGCGGCTGTGAG 962
Db 901 CTTGGCCGCTACTCTTTTCCCTCTCTCTGGGCTCTCCCACTCTGGGCGGCTGTGAG 960
QY 963 CTTACCTGAGCCCTGAGCTGGGCGCAGCTGCCAAGTTCAGGCGCTGTCTCT 1016
Db 961 CTTACCTGAGCCCTGAGCTGGGCGCAGCTGCCAAGTTCAGGCGCTGTCTCT 1014
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RESULT 3
AL578261/c 932 bp mRNA linear EST 07-APR-2004
LOCUS AL578261 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
DEFINITION CDNA clone CS0DK002YM07 3-PRIME, mRNA sequence.

ACCESSION AL578261
VERSION AL578261.3 GI:46257165
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE Li.W.B., Gruber.C., Jessee.J. and Polayes.D.
JOURNAL Full-length cDNA libraries and normalization
COMMENT Unpublished (2001)

On Feb 16, 2001 this sequence version replaced gi:31316478.
Contact: Genoscope
Genoscope - Centre National de Sequenage
2 rue Gaston Crémieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
8290.f

For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?c=CS0DK002AG04NP1&c=8290.f.

FEATURES
source
1..932
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DK002YM07"
/cell_type="HELA CELLS COT 25-NORMALIZED"

/cell_line="HELA"
/clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 82.6%; Score 908.4; DB 1; Length 932;
Best Local Similarity 98.6%; Pred. No. 2e-217;
Matches 910; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 84 CGCAGGAGGCGCGCGTATATCAGGACCATGCGCGCGACCGGTCATCACCTCGCGCATCG 143
Db 932 CGCAGGAGGCGCGCGTATATCAGGACCATGCGCGCGACCGGTCATCACCTCGCGCATCG 873
QY 144 TGGGTGAGAGGAGCGCGAACTCGGGCGTTGGCGGTGGCGGTGGCAGGGGAGGCTGCGCTGTGGG 203
Db 872 TGGGTGAGAGGAGCGCGAACTCGGGCGTTGGCGGTGGCGGTGGCAGGGGAGGCTGCGCTGTGGG 813
QY 204 ATTCCACGATATGCGGAGTGAGCTGCTCAGCCACCGCTGGGCACTCACGGCGCGCACT 263
Db 812 ATTCCACGATATGCGGAGTGAGCTGCTCAGCCACCGCTGGGCACTCACGGCGCGCACT 753
QY 264 GCTTTGAAACCTATAGTGACCTTAGTGATCCCTCCGGGTGGATGGTCCAGTTGGCCAGC 323
Db 752 GCTTTGAAACCTATAGTGACCTTAGTGATCCCTCCGGGTGGATGGTCCAGTTGGCCAGC 693
QY 324 TGACTTCATGCGCCCTCGTACCTGGGGAATTCACCTATGACATTCGCTTGGTGAAGC 443
Db 692 TRACTTCATGCGCCCTCGTACCTGGGGAATTCACCTATGACATTCGCTTGGTGAAGC 633
QY 384 ATATCTATCTGAGCCCTCGTACCTGGGGAATTCACCTATGACATTCGCTTGGTGAAGC 443
Db 632 ATATCTATCTGAGCCCTCGTACCTGGGGAATTCACCTATGACATTCGCTTGGTGAAGC 573
QY 444 TGTCTGACCTGTGACCTACACTAAACACATCAGGCCCATCTGTCTCAGGCGCTCCACAT 503
Db 572 TGTCTGACCTGTGACCTACACTAAACACATCAGGCCCATCTGTCTCAGGCGCTCCACAT 513
QY 504 TTGAGTTTGAGAACCGGACAGACTGCTGGGTGAGTGGCTGGGGGTATCAAAAGAGGATG 563
Db 512 TTGAGTTTGAGAACCGGACAGACTGCTGGGTGAGTGGCTGGGGGTATCAAAAGAGGATG 453
QY 564 AGGCACCTGCCATCTTCCCCACACCTCCAGGAAGTTTCAGGTCCGCTCATATAAACAACCTCTA 623
Db 452 AGGCACCTGCCATCTTCCCCACACCTCCAGGAAGTTTCAGGTCCGCTCATATAAACAACCTCTA 393
QY 624 TGTGCAACCACTCTTCTCAAGTACAGTTTCGGCAAGGACATCTTTGGAGACATGTTT 683
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QY 684 GTGCTGGCAATGCCAAGGCGGGAAGATGCTTCCGTTCCGTTAACTCAGGTGGACCTTGG 743
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QY 744 CCTGTAAACAGGATGGAAGTGTGATCAGATTGGAGTCTGAGCTGGGAGTGGGCTGTG 803
Db 272 CCTGTAAACAGGATGGAAGTGTGATCAGATTGGAGTCTGAGCTGGGAGTGGGCTGTG 213
QY 804 GTGCGCCCAATCGCGCGGCTGTCTACACCAATATCAGCCACCACTTTGAGTGGATCCAGA 863
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QY 864 AGCTGATGGCCAGAGTGGCATGTCCAGCGCAGACCCCTCTGCGCGCTACTCTTTTTC 923
Db 152 AGCTGATGGCCAGAGTGGCATGTCCAGCGCAGACCCCTCTCTGCGCGCTACTCTTTTTC 93
QY 924 CTCTTCTCTGCGCTCTCTCCCACTCTCTGCGCGGCTGTGAGCTACTCTGAGCCCATGCGAGCC 983
Db 92 CTCTTCTCTGCGCTCTCTCCCACTCTCTGCGCGGCTGTGAGCTACTCTGAGCCCATGCGAGCC 33
QY 984 TGGGGCCACTGCGCAAGTTCAGGCC 1006

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Db 32 TGGGGCCACTGCGCAAGNACGCC 10 |||||
RESULT 4
AL555870 884 bp mRNA linear EST 30-MAR-2004
LOCUS AL555870 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
DEFINITION CDNA clone CSODK002YM07 5-PRIME, mRNA sequence.
ACCESSION AL555870
VERSION AL555870.3 GI:45860593
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS 1 (bases 1 to 884)
TITLE Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
JOURNAL Full-length cDNA libraries and normalization
COMMENT Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:31277675.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
8290.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSODK002AG040P1&c=8290.f.
FEATURES
source
1..884
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="CSODK002YM07"
/cell_line="HELA"
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/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Query Match 79.1%; Score 870.4; DB 1; Length 884;
Best Local Similarity 99.8%; Pred. No. 7.1e-208;
Matches 882; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 3 CGGGAGAGGAGCCATGGCGCGCGCGCGCTGCTGCTGGCGCTCTGCTGGCTGGG 62
Db 1 CGGGAGAGGAGCCATGGCGCGCGCGCGCTGCTGCTGGCGCTCTGCTGGCTGGG 60
QY 63 CTGGACTCAGGAAGCCGCGAGTCGCGAGGCGCGCGCT-TATCAGACCATCGGCCGA 121
Db 61 CTGGACTCAGGAAGCCGAGTCGCGAGGCGCGCGCTGCTGCTGAGACCATCGGCCGA 120
QY 122 CGGGTCTACAGTCGCGCATCTGGGTGGAGAGAGAGCCCGAACTCGGGCGTTGGCGTGG 181
Db 121 CGGGTCTACAGTCGCGCATCTGGGTGGAGAGAGAGCCCGAACTCGGGCGTTGGCGTGG 180
QY 182 CAGGGAGCTCGCGCTGTGGATTCCACGTATGCGAGTGAGCTGCTCAGCCACCGC 241
Db 181 CAGGGAGCTCGCGCTGTGGATTCCACGTATGCGAGTGAGCTGCTCAGCCACCGC 240
QY 242 TGGGCACTCAGCGCGCGCACTGCTTTTGAACCTATAGTACCTTAGTGATCCCTCGGG 301
Db 241 TGGGCACTCAGCGCGCGCACTGCTTTTGAACCTATAGTACCTTAGTGATCCCTCGGG 300
QY 302 TGGATGTCAGTTTGGCCAGCTGACTTCATGCGCATCTCTTGGAGCCTGCGAGCCCTAC 361
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361 TACACCCGTTACTTTCGTATCGAATATCTATCTGAGCCCTCGGTACCTGGGGAATTCACCC 420
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422 TATGACATTCCTTGGTGAAGCTGTCTGACCTGTCTACCTACCTAAACACATCCAGCCC 481
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481 ATCTGTCTCAGCCCTCCACATTTGAGTTTGAGACCGGACAGACTGCTGGGTGACTGGC 540
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601 GTGCCCATCAAAACAACTCTATGTGCAACCACTCTTCTCAAGTACAGTTTCCGCAAG 660
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661 GACATCTTTGGAGACATGCTTTGCTGCGCAATGCCAAGCGGGAAGTGCCTGCTTC 720
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722 GGTGACTCAGGTGGACCTTGGCTGTAAACAAGGATGGACTGTGGTATCAGATTGGAGTC 781
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721 GGTGACTCAGGTGGACCTTGGCTGTAAACAAGGATGGACTGTGGTATCAGATTGGAGTC 780
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782 GTGAGCTGGGGAGTGGCTGTGCTGCGCCCAATCGGCCCGGTCTTACACCAATATCAGC 841
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781 GTGAGCTGGGGAGTGGCTGTGCTGCGCCCAATCGGCCCGGTCTTACACCAATATCAGC 840
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842 CACCACCTTTGAGTGGATCCAGAGCTGATGGCCGAGTGGCAT 885
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841 CACCACCTTTGAGTGGATCCAGAGCTGATGGCCGAGTGGCAT 884
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RESULT 5
BX417595 1057 bp mRNA linear EST 01-MAY-2004
LOCUS BX417595 Homo sapiens PLACENTA Homo sapiens cDNA clone CSODE010YF05
DEFINITION 5-PRIME, mRNA sequence.
ACCESSION BX417595
VERSION BX417595.2 GI:46933208
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 1057)
JOURNAL Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
COMMENT Full-length cDNA libraries and normalization
Unpublished (2001)
On May 13, 2003 this sequence version replaced gi:30654423.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 8290.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSODE010CH03QP1&c=8290.f.
FEATURES
source
1..1057
/organism="Homo sapiens"
/mol_type="mRNA"
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/db_xref="taxon:9606"
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/tissue_type="PLACENTA"
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/notes="Vector: pCMWSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with NotI and cloned into
the NotI and EcoRV sites of the pCMWSPORT 6 vector.
Library was not normalized."

```

ORIGIN

Query Match	78.7%	Score	866	DB 5	Length	1057			
Best Local Similarity	95.3%	Pred. No.	9,4e-207						
Matches	942	Conservative	13	Mismatches	23	Indels	10	Gaps	6

QY	1	CGCGGAGAGGAGCCATGGCGCGCGCGGGCGCGCTGCTGGCGCTGCTGGCGCTGCTGGCGCTG	60
Db	3	CGCGGAGAGGAGCCATGGCGCGCGCGGGGC-STGCTCTGGCGCTGCTGGCGCTG	61
QY	61	GGCTGGACTCAGGAAGCCGGAGTTCGACGAGGCGGCGCGCT-TATCAGGACCATCGCGCC	119
Db	62	GGCTGGACTCAGGAAGCCGGAGTTCGACGAGGCGGCGCGCTTATCAGGACCATCGCGCC	121
QY	120	GACGGGTATCATCGTTCGCGCATCGTGGTGGAGAGGACGCCGAACCTCGGCGTGGCGCGT	179
Db	122	GACGGGTATCATCGTTCGCGCATCGTGGTGGAGGAGCGCGAACTCGGCGCTGGCGCT	181
QY	180	GGCAGGGGAGCTGCGGCTGTGGATTCACAGTATCGGAGTGTAGCGTCTCAGCCACC	239
Db	182	GGCAGGGGAGCTGCGGCTGTGGGATTCACAGTATCGGAGTGTAGCGTCTCAGCCACC	241
QY	240	GCTGGGCACCTCACGGCGGGCGACCTGCTTTGAAACCTATAGTGACCTTAGTGATCCCTCG	299
Db	242	GCTGGGCACCTCACGGCGGGCGACCTGCTTTGAAACCTATAGTGACCTTAGTGATCCCTCG	301
QY	300	GGTGGATGTCTCCAGTTTGGCAGCTGACTTCCATGCCATCTCTTCGAGGCTCGCAGGCT	359
Db	302	GGTGGATGTCTCCAGTTTGGCAGCTGACTTCCATGCCATCTCTTCGAGGCTCGCAGGCT	361
QY	360	ACTACACCGGTTACTTGGTATCGAAATATCTATCTGAGCCCTCGCTACCTCGGGAAATTCAC	419
Db	362	ACTACACCGGTTACTTGGTATCGAAATATCTATCTGAGCCCTCGCTACCTCGGGAAATTCAC	421
QY	420	CCTATGACATTCGCTTGGTGAAGCTGTCTGCACTGTACCTACCTACATAAACACATCCAGC	479
Db	422	CCTATGACATTCGCTTGGTGAAGCTGTCTGCACTGTACCTACCTACATAAACACATCCAGC	481
QY	480	CCATCTGTCTCCAGGCTCCACATTTGAGTTTCGAGAACCGGACAGACTGTGGTGGACTG	539
Db	482	CCATCTGTCTCCAGGCTCCACATTTGAGTTTCGAGAACCGGACAGACTGTGGTGGACTG	541
QY	540	GCTGGGGGTACATCAAGAGGATGAGGCACTGCCATCTCCCCACACCTCCAGGAAGTTC	599
Db	542	GCTGGGGGTACATCAAGAGGATGAGGCACTGCCATCTCCCCACACCTCCAGGAAGTTC	601
QY	600	AGGTCCGCATCAATAACACTTATGTGCAACCACTTCTTCTCAAGTACAGTTTCGCA	659
Db	602	AGGTCCGCATCAATAACCACTTATGTGCACTTCTTCTTCTCAAGTACAGTTTCGCA	660
QY	660	AGGACATCTTTGAGACATGGTTTGTCTGGCAATGCCAAGCGGGAGGATGCCTGCT	719
Db	661	A-GACATCTTTGAGACATGGTTTGTCTGGCAATGCCAAGCGGGAGGATGCCTGCT	719
QY	720	TCGGTGACTCAGGTGGACCTTCGGCTGTAAACAGGATGGACTGTGTATCAGATGGAG	779
Db	720	TCGGTGACTCAGGTGGACCTTCGGCTGTAAACAGGATGGACTGTGTATCAGATGGAG	779
QY	780	TCGTGAGCTGGGAGTGGGCTGTGGTTCGGCCCAATCGGCCCGGTGTCTACCAAAATATCA	839
Db	780	TYGTGAGCTGGGAGTGGGCTGTGGTTCGGCCCAATCGGCCCGGTGTCTACCAAAATATCA	839
QY	840	GCACCACTTTGATGGATCCAGAAGCTGATGCCCCAGAGTGGCATGTCCAGCCAGACC	899

Db	840	GCACCACTTTGAGTGGATCCAGAAAGCTGATGCCCCAGAGTGGCATGTGCCAGCCAGACC	899
Qy	900	CTCTCCCTGGCGCTACTCTTTTCCCTCTCTCTCTGGGCTCTCCCACTCTCTGGGCGCGGTCT	959
Db	900	CTYCTKGC--GCTATYTTTTTCCCTCTCTCTYTGCGGTCTCC-----ACTCTKGGCGGGY	953
Qy	960	GAGCCTACTCTGAGCCCATGAGCCTGGG	987
Db	954	TGAGCTWACTGAGCCMATGCASCCTGGGG	981
RESULT 6			
EX454526/c			
LOCUS	EX454526	Homo sapiens	898 bp mRNA .linear EST 05-MAY-2004
DEFINITION	3-PRIME, mRNA sequence.		
ACCESSION	EX454526		
VERSION	EX454526		
KEYWORDS	EX454526.1	GI:31019139	
SOURCE	EST.		
ORGANISM	Homo sapiens (human)		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (bases 1 to 898)		
JOURNAL	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.		
COMMENT	Full-length cDNA libraries and normalization		
	Unpublished (2001)		
	Contact: Genoscope		
	Genoscope - Centre National de Sequencage		
	2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE		
	Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr		
	1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime		
	end enriched, double-strand cDNA was digested with Not I and cloned		
	into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library		
	was not normalized. Library was constructed by Life Technologies, a		
	division of Invitrogen.		
	This sequence belongs to sequence cluster 8290.f		
	For more information about this cluster, see		
	http://www.genoscope.cns.fr/cdna?e=CS0BAK026CB01NM1&c=8290.f.		

FEATURES
source

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DE010YP05"
/tissue_type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched, into
double-strand cDNA was digested with Not I and cloned, into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

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ORIGIN

Query Match	71.0%;	Score 780.6;	DB 5;	Length 998;
Best Local Similarity	96.5%;	Pred. No. 2.8e-185;		
Matches 862;	Conservative 0;	Mismatches 24;	Indels 7;	Gaps 6;
QY	184	GGGGAGCCTGCGCCTGTGGGATT--CCACAGCTATCGGAGTGA-GCCTGCTCAGCCACCG	240	
Db	893	GGAAACCCGGCGCCTTTGGGATTTCCCCCGTATCGAAGTGAGGCTTGCTCAGGCCCG	834	
QY	241	CT--GGGCACCTCAGCGGG--CGCACCTGCTTTGAAA CCTATAGTGA CCTTATGTA TCCCTCC	298	
Db	833	TTGGGGCACTCCCGCGCGCGCTGCTTTTGAACCTATAGTGA CCACTTAAGTGA TCCCTCC	774	
QY	299	GGGTGATGGTTCAGTPTTGGCCAGCTGACTTCATGCCATCCTTCTGGAGCCTGCAGGCC	358	
Db	773	GGTGGATGGTTCAGTPTTGGCGAGCTGACTTCCATGCCATCTTCTGGAGCCTGCAGGCC	714	
QY	359	-TACTACACCCGTTACTTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGGAATTC	417	
Db	713	TTACTACACCCGTTCTTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGGAATTC	654	

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Qy 418 A-CCCTATGACATTGCTTGGTGAAGCTGTCTGCACTGTCACTTACCTACCTA CACTAAACACATCC 476
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Db 653 ACCCTATGACATTGCTTGGTGAAGCTGTCTGCACTGTCACTTACCTA CACTAAACACATCC 594
|
Qy 477 AGCCCTCTCTCCAGGCTCCACATTTGAGTTTGAGACCGGACAGACTGCTGGTGA 536
|
Db 593 AGCCCTCTCTCTCCAGGCTCCACATTTGAGTTTGAGACCGGACAGACTGCTGGTGA 534
|
Qy 537 CTGCTGGGGTACATCAAGAGAGATGAGGACCTGCTGCTTCCACACACCTCCAGGAAG 596
|
Db 533 CTGCTGGGGTACATCAAGAGAGATGAGGACCTGCTGCTTCCACACACCTCCAGGAAG 474
|
Qy 597 TTCAGGTGCGCCATCAATAAACACTCTATGTGCAACCACTCTTCTCTCAAGTACAGTTTC 656
|
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|
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|
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|
Qy 777 GAGTCGTGAGCTGGGGAGTGGGCTGTGCTCGGCCAAATCGGCCCGGTGTCTACACCAATA 836
|
Db 293 GAGTCGTGAGCTGGGGAGTGGGCTGTGCTCGGCCAAATCGGCCCGGTGTCTACACCAATA 234
|
Qy 837 TCAGCCACCATTGAGTGATCAGAAAGCTGATGGCCAGAGTGGGATGCTCCAGGCGAG 896
|
Db 233 TCAGCCACCATTGAGTGATCAGAAAGCTGATGGCCAGAGTGGGATGCTCCAGGCGAG 174
|
Qy 897 ACCCTCTGCGCGCTACTCTTTTCCCTCTCTCTGCGCTCTCCACTCTCGGGCGG 956
|
Db 173 ACCCTCTGCGCGCTACTCTTTTCCCTCTCTCTGCGCTCTCCACTCTCGGGCGG 114
|
Qy 957 TCTGAGCCTACCTGAGCCCACTGAGCCTGGGGCACTGCCAAGTCAAGCCCTGTTCTCT 1016
|
Db 113 TCTGAGCCTACCTGAGCCCACTGAGCCTGGGGCACTGCCAAGTCAAGCCCTGTTCTCT 54
|
Qy 1017 TCTGCTCTGTTGTTAATAACACATTTCCAGTTGATGCTTGCAGGCGCATTTT 1069
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Db 53 TCTGCTCTGTTGTTAATAACACATTTCCAGTTGATGCTTGCAGGCGCATTTCT 1

RESULT 7
BI334059 871 bp mRNA linear EST 30-JUL-2001
LOCUS 602997320F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5139509 5',
DEFINITION mRNA sequence.
ACCESSION BI334059
VERSION BI334059.1 GI:15018703
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 871)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L14M11343 row: h column: 06
High quality sequence stop: 826.
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    /clone="IMAGE:5139509"
    /tissue_type="cervical carcinoma cell line"
    /lab_host="DH10B"
    /clone_lib="NIH MGC 12"
    /notes="Organ: cervix; Vector: pCMV-SPORT6; Site 1: NotI;
    Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr.
    Average insert size 1.4 kb. Library prepared by Life
    Technologies."
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ORIGIN

Query Match 70.7%; Score 777.2; DB 4; Length 871;
Best Local Similarity 97.9%; Pred. No. 2e-184;
Matches 842; Conservative 0; Mismatches 8; Indels 10; Gaps 5;

Qy 186 GGAGCCTGCGCTGTGGGATTCACGATGCGGAGTGAAGCTGCTCAGCCACCGCTGGG 245
|
Db 1 GGAGCCTGCGCTGTGGGATTCACGATGCGGAGTGAAGCTGCTCAGCCACCGCTGGG 60
|
Qy 246 CACTCAGCGGGCGCACTGCTTTGAAACCTATAGTGAACCTTAGTGATCCCTCCGGGTGA 305
|
Db 61 CACTCAGCGGGCGCACTGCTTTGAAAC-----TGACCTTAGTGATCCCTCCGGGTGA 114
|
Qy 306 TGGTCCAGTTTGGCCAGCTGACTTCCATGCGCATCTTCTGGAGCCTGCAGGCCTACTACA 365
|
Db 115 TGGTCCAGTTTGGCCAGCTGACTTCCATGCGCATCTTCTGGAGCCTGCAGGCCTACTACA 174
|
Qy 366 CCGTTACTTCGATCGAATATCTATCTGAGCCTCGCTACCTGGGGAATTCACCTATG 425
|
Db 175 CCGTTACTTCGATCGAATATCTATCTGAGCCTCGCTACCTGGGGAATTCACCTATG 234
|
Qy 426 ACATTGCTTGGTGAAGCTGTCTGACCTGTACCTACACTAAACATCCAGCCATCT 485
|
Db 235 ACATTGCTTGGTGAAGCTGTCTGACCTGTACCTACACTAAACATCCAGCCATCT 294
|
Qy 486 GTCTCCAGGCTCCACATTTGAGTTTGAGAACCGGACAGACTCTGGGTGACTTGGGTGGG 545
|
Db 295 GTCTCCAGGCTCCACATTTGAGTTTGAGAACCGGACAGACTCTGGGTGACTTGGGTGGG 354
|
Qy 546 GGTACATCAAGAGATGAGGACCTGCCATCTCCCCACACCTCCAGGAAGTTCAAGTGC 605
|
Db 355 GGTACATCAAGAGATGAGGACCTGCCATCTCCCCACACCTCCAGGAAGTTCAAGTGC 414
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Qy 606 CCATCATAAACACTCTATGTGCAACCACTCTTCTCAAGTACAGTTTCCGCAAGGACA 665
|
Db 415 CCATCATAAACACTCTATGTGCAACCACTCTTCTCAAGTACAGTTTCCGCAAGGACA 474
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Qy 666 TCTTTGGAGACATGTTTGTGCTGGCAATGCCCAAGCGGGAAGGATGCTGCTCGGTG 725
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|
Qy 905 TGGCCGCTACTCTTTTCCCTCTTCTCTGGGTCTCTCCACTCTCTGGGCGCGGTCTAGCC 964
|
Db 715 TGGCCG-TACTCTTTTCCCTCTTCTCTGGGTCTCTCCACTCTCTGGGCGCGGTCTAGCC 773
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Qy 965 TACTGAGCCCATGCAAGCTTGGGGCGCTGCGCAAGTCAAGCCCTGTTCTTCTTCTTCT 1024
|


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Db      774  TAACTGAGCCCATGCGGCGGCACTG-CAAGTCAGGCCCTGGTTCCTCTGACTT 832
Qy      1025 GTTTGGTAATAAACACATTC 1044
Db      833  G-TAGGTAATAAAAAACATTC 851

RESULT 8
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LOCUS   602970095F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5109695 5',
DEFINITION mRNA sequence.
ACCESSION BI259237.1 GI:14816376
VERSION   1
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 777)
AUTHORS  NIH-MGC http://mgc.nci.nih.gov/.
TITLE    National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL  Unpublished (1999)
COMMENT  Contact: Robert Strausberg, Ph.D.
         Tissue Procurement: ATCC
         cDNA Library Preparation: Life Technologies, Inc.
         cDNA Library Arrayed by: Incyte Genomics, Inc.
         DNA Sequencing by: Incyte Genomics, Inc.
         Clone distribution: MGC clone distribution information can be
         found through the I.M.A.G.E. Consortium/LLNL at:
         http://image.llnl.gov
         Plate: LLAM11265 row: m column: 24
         High quality sequence stop: 777.

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         Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
         Average insert size 1.4 kb. Library prepared by Life
         Technologies."

ORIGIN
Query Match 69.1%; Score 760.4; DB 4; Length 777;
Best Local Similarity 99.7%; Pred. No. 3.3e-180;
Matches 772; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy      68  CTCAGGAAGCCGGAGTCGACGAGGCGCGCGTATCAGACCATCGCGCCGACGGGTC 127
Db      1  CTCAGGAAGCCGGAGTCGACGAGGCGCGCGTATCAGACCATCGCGCCGACGGGTC 60

Qy      128 ATACGTCGCGCATCGTGGGTGGAGAGGACGCCGAACCTCGGGCTTCGCGTGGCAGGG 187
Db      61 ATACGTCGCGCATCGTGGGTGGAGAGGACGCCGAACCTCGGGCTTCGCGTGGCAGGG 120

Qy      188 AGCCTGCGCTGTGGGATTCACGATATGCGAGTGAGCGCTGCTCAGCACCGCTGGGCA 247
Db      121 AGCCTGCGCTGTGGGATTCACGATATGCGAGTGAGCGCTGCTCAGCACCGCTGGGCA 180

Qy      248 CTCACGGCGGCGCATCGCTTTTGAACCTATAGTACCTTAGTATGATTCCTCGGGTGGATG 307
Db      181 CTCACGGCGGCGCATCGCTTTTGAACCTATAGTACCTTAGTATGATTCCTCGGGTGGATG 240

Qy      308 GTCCAGTTTGGCCAGCTGACTTCCATGCCATCTTCTGGAGCTTCGAGGCTACTACACC 367
Db      241 GTCCAGTTTGGCCAGCTGACTTCCATGCCATCTTCTGGAGCTTCGAGGCTACTACACC 300

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Qy      368 CGTTACTTCTGATCGAATATCTATCTGAGCGCTCGCTACCTGGGGAATTCACCCCTATGAC 427
Db      301 CGTTACTTCTGATCGAATATCTATCTGAGCGCTCGCTACCTGGGGAATTCACCCCTATGAC 360

Qy      428 ATTGCCCTTGGTGAAGCTGTCTGCACCTGTGCACCTTACACATAAACACATCCAGCCCATCTGT 487
Db      361 ATTGCCCTTGGTGAAGCTGTCTGCACCTGTGCACCTTACACATAAACACATCCAGCCCATCTGT 420

Qy      488 CTCAGCGCTCCCATTCATTGAGTTTGAAGACCGGACAGACTGCTGGGTGACTTGGCTGGGG 547
Db      421 CTCAGCGCTCCCATTCATTGAGTTTGAAGACCGGACAGACTGCTGGGTGACTTGGCTGGGG 480

Qy      548 TACATCAAGAGGATGAGGCACTGCCATCTCCCCACACCCCTCCAGGAAGTTTCAGGTGCCC 607
Db      481 TACATCAAGAGGATGAGGCACTGCCATCTCCCCACACCCCTCCAGGAAGTTTCAGGTGCCC 540

Qy      608 ATCATCAACAACTCTATGTGCAACCACTCTTCTCAAGTACAGTTTCCGCAAGGACATC 667
Db      541 ATCATCAACAACTCTATGTGCAACCACTCTTCTCAAGTACAGTTTCCGCAAGGACATC 600

Qy      668 TTTGGAGACATGTTTGTGCTGGCAATGCCAAGCGGGAAGGATGCTTCTCGGTGAC 727
Db      601 TTTGGAGACATGTTTGTGCTGGCAATGCCAAGCGGGAAGGATGCTTCTCGGTGAC 660

Qy      728 TCAGGTGGACCCCTTGGCCTGTAAACAGGATGAGACTGTGGTATCAGATTGAGTCTGTGAC 787
Db      661 TCAGGTGGACCCCTTGGCCTGTAAACAGGATGAGACTGTGGTATCAGATTGAGTCTGTGAC 720

Qy      788 TGGGGAGTGGCTGTGTCGCGCCCAATCGCCGCTGTCTACACCAATATCAGC 841
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DEFINITION mRNA sequence.
ACCESSION BI27608
VERSION   BI27608.1 GI:15939145
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 878)
AUTHORS  NIH-MGC http://mgc.nci.nih.gov/.
TITLE    National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL  Unpublished (1999)
COMMENT  Contact: Robert Strausberg, Ph.D.
         Email: cgapbs-remail.nih.gov
         Tissue Procurement: Life Technologies, Inc.
         cDNA Library Preparation: Life Technologies, Inc.
         cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
         DNA Sequencing by: Incyte Genomics, Inc.
         Clone distribution: MGC clone distribution information can be
         found through the I.M.A.G.E. Consortium/LLNL at:
         http://image.llnl.gov
         Plate: LLAM11411 row: e column: 19
         High quality sequence stop: 828.

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         /tissue_type="medulla"
         /lab_host="DH10B"
         /clone_lib="NIH_MGC_119"
         /note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
         Site 2: EcoRV (destroyed); RNA source normal medulla from
         anonymous male age 27. Library is oligo-dr primed and
         directionally cloned (EcoRV site is destroyed upon

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cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH MGC Library."

Query Match					
		66.7%;	Score 733.6;	DB 4;	Length 878;
		Best Local Similarity 93.7%;	Pred. No. 1.9e-173;		
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QY	39	TGCTGGCGCTGCTGCTGGCTTGGACTCGAGAACCCGGAGTCGCAGGAGCGCGGC	98		
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QY	99	CGTTATTAGAACCATCGCGGCCGACGGGTTCATCAGTCGCGCATCGTGCGTGGGTGGAGAGGACG	158		
DB	61	CGTTATTAGAACCATCGCGGCCGACGGGTTCATCAGTCGCGCATCGTGCGTGGGTGGAGAGGACG	120		
QY	159	CCGAACCTGGGGCGTTGGCCGTGGCAGGGGAGCTGCGCCCTGTGGGATTCACCACTATGCG	218		
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QY	219	GAGTAGCCTGCTCAGCACACCGCTGGGCACCTCAGCGGGGSCACTGCTTTGAAACCCTATA	278		
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QY	279	GTGACCTTAGTGATCCCTCCGGGTGGGATGGTFCAGTTTGGCCAGCTGACATTCATGCGCAT	338		
DB	235	-TGACCTTAGTGATCCCTCCGGGTGGGATGGTFCAGTTTGGCCAGCTGACATTCATGCGCAT	293		
QY	339	CCTTCTGAGGCTGACGSGCTACTACACCGTTACTTCTGATCCAAATATCTATCTGAGCC	398		
DB	294	CCTTCTGAGGCTGACGSGCTACTACACCGTTACTTCTGATCCAAATATCTATCTGAGCC	353		
QY	399	CTCGTACCTGGGGAATTCACCTPATGACAATGCTTGGTGAAGCTGTCTGCACCTGTCA	458		
DB	354	CTCGTACCTGGGGAATTCACCTPATGACAATGCTTGGTGAAGCTGTCTGCACCTGTCA	413		
QY	459	CCTACACTAACAACATCCAGCCCATCTGCTCCAGGCGCTCCACATTTGAGTTTGAAGAACC	518		
DB	414	CCTACACTAACAACATCCAGCCCATCTGCTCCAGGCGCTCCACATTTGAGTTTGAAGAACC	473		
QY	519	GGACAGACTGCTGGGTGACTGGCTGGGGGTAATCAAAGAGGATGAGGCATGCGCATCTC	578		
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QY	699	AAGCGGGGAAGGATGCTGCTTGGTGAATCAGTGGACCTTGGCCCTGTAAACAAGA--	756		
DB	628	AAGCGGGGAAGGATGCTGCTTGGTGAATCAGTGGACCTTGGCCCTGTAAACAAGAA	687		
QY	757	TGACTGTGGTATCAGATTTGAGTCGTGAGCTGGGGAGTGGGCTGTGGTGGGCCCAA - TC	815		
DB	688	TGACTGTGGTATCAGATTTGAGTCGTGAGCTGGGGAGTGGGCTGTGGTGGGCCCAAATTC	747		
QY	816	GGCCCGGTGTCTACCAATATACGCCACCACTTTTGAG - TGGAATCCAGAAGCTGATGCC	874		
DB	748	GGCCCGGTGTCTACCAATATACGCCACCACTTTTGAGTTGGATCCAGAAGCTGATGCC	807		
QY	875	CAGATGGCATGTCCCAGGACAG - ACCCCTCTCTGGCCGCTACTCTTTTTTCCCTCTCTCTG	933		
DB	808	CAGATGGCATGTCCCAGGACCAACCCCTCTCTGGCCATATTCTTTTTTCCCTCTCTCTG	867		
QY	934	GGCTCTCCCCA	943		

D_b 868 GGCTCTTCCA 877

RESULT 10
CB529999/c

LOCUS	DEFINITION
CB329993/C	

ACCESSION

VERSION
KEYWORDS

SOURCE ORGANISM

REFERENCE

[illegible]JOURNAL
CONTENT

COMMENT

FEATURES

1
1
4
9
16

ORIGIN

Query Ma
Post. 100

BEST LOC Matches

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 UI-H-F72-bj1-b-24-0-UI.s1 NCI CGAP F72 Homo sapiens cDNA clone
 UI-H-F72-bj1-b-24-0-UI 3', mRNA sequence.
 CB529999
 CB529999.1 GI:29391246
 EST.
 Homo sapiens (human)
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 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 743)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Dr. Gary W. Hunninghake, U of I
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/cgap.html>
 seq primer: M13 FORWARD
 POLYA=Yes.

Location/Qualifiers

1. 743

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/clone_lib="NCI CGAP FT2"

/note="organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI CGAP FT2 is a subtracted cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was subtracted according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

TAG TISSUE=Human Lung Alveolar Macrophage

TAG LIB=UI-H-FT2

TAG SEO=GGCATGCCG"

Index	Score	DB	Length
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723; Conservative	94.1%	Pred. No. 2.1e-157;	
0; Mismatches	3	Indels	42
Gaps	1		

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Db 743 CTTAGTATCCCTCCGGGTGATGTCAGTTTGGCAGCTGACTTCCATGCCATCTTC 684
Qy 344 TGGAGCCTGCGAGGCTACTACACCGGTTACTTCGTATCGAATATCTATCTGAGCCCTCGC 403
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Qy 404 TACCTGGGGAATACCTATGACATTCCTGTTGGTGAAGCTGTCTGACCTGTCACTTAC 463
Db 623 TACCTGGGGAATACCTATGACATTCCTGTTGGTGAAGCTGTCTGACCTGTCACTTAC 564
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Db 503 GACTGCTGGGTGACTGCTGGGGGTACATCAAGAGGATGAGGCACTGCCATCTCCCCAC 444
Qy 584 ACCCTCCAGGAAGTTGAGTCCGATCATAAACAACTCTATGTGCAACCACTTCTTCTC 643
Db 443 ACCCTCCAGGAAGTTGAGTCCGATCATAAACAACTCTATGTGCAACCACTTCTTCTC 384
Qy 644 AAGTACAGTTTCCGCAAGGACATCTTTGGAGACATGTTTGTGGCAATGCCCAAGGC 703
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Qy 704 GGAAGGATGCTGCTCGGTGACTCAGGTGACCTTGGGCTGTAAACAGGATGGAATG 763
Db 347 -----GGTACTCAGTGGACCTTTGGGCTGTAAACAGGATGGAATG 306
Qy 764 TGGTATCAGATTGGAGTCTGAGCTGGGAGTGGGCTGTGGTGGCCCAATCGGCCCGGT 823
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Qy 824 GTCTACCAATATCAGCACCATCTTGGAGTGATCCAGAGCTGATGGCCCAAGTGGC 883
Db 245 GTCTACCAATATCAGCACCATCTTGGAGTGATCCAGAGCTGATGGCCCAAGTGGC 186
Qy 884 ATGTCCAGCAGACCCCTCTGCGGCTACTCTTTTCCCTTCTCTGCGGCTCTCCCA 943
Db 185 ATGTCCAGCAGACCCCTCTGCGGCTACTCTTTTCCCTTCTCTGCGGCTCTCCCA 126
Qy 944 CTCCTGGGCGGCTGAGCCTACCTGAGCCCATGACGCTGGGCGCACTGCCAAGTCA 1003
Db 125 CTCCTGGGCGGCTGAGCCTACCTGAGCCCATGACGCTGGGCGCACTGCCAAGTCA 66
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Db 65 GCCCTGTTCTCTGCTGTTGTTGGTAATAACACATTCAGTTGA 18
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RESULT 11
LOCUS A1126185
DEFINITION A1126185 633 bp mRNA linear EST 28-OCT-1998
3' similar to SW.F588_HUMAN Q16651 PROSTASIN PRECURSOR ;, mRNA
sequence.
ACCESSION A1126185
VERSION A1126185.1 GI:3594699
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo;
1 (bases 1 to 633)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
```

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image.html
Insert length: 912 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 455.
Location/Qualifiers
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/sex="male"
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/clone_lib="Soares testis NHT"
/notes="Vector: pT73D-Fac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT) primer [5].
TGTACCAATCTGAAGTGGAGCGCGCCCAATTTTTTTTTT 3'.
Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

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Query Match 56.8%; Score 624.8; DB 1; Length 633;  
Best Local Similarity 99.4%; Pred. No. 4.3e-146;  
Matches 626; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
Qy 425 GACATTCCTTGGTGAAGCTGTCTGACCTGTCACTACACTAAACATCCAGCCCATC 484  
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Qy 485 TGTCTCAGAGCTCCACATTTGAGTTTGAACCGGACAGACTGCTGGGTGACTGGCTGG 544  
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Qy 545 GGGTACATCAAGAGGATGAGGCACTGCCATCTCCCAACCCCTCCAGGAAGTTGAGT 604  
Db 513 GGGTACATCAAGAGGATGAGGCACTGCCATCTCCCAACCCCTCCAGGAAGTTGAGT 454  
Qy 605 GCCATCAATAAACACTCTATGTGCAACCACTCTTCTCAAGTACAGTTTCCGCAAGGAC 664  
Db 453 GCCATCAATAAACACTCTATGTGCAACCACTCTTCTCAAGTACAGTTTCCGCAAGGAC 394  
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Db 393 ATCTTTGGAGACATGTTTGTGCTGGCAATGCCAAGCGGGAAGGATGCTGCTCGGT 334  
Qy 725 GACTCAGTGGAGCCCTTGGCTGTAAACAAGATGGAATGCTGTATCAGATTGAGTGGT 784  
Db 333 GACTCAGTGGAGCCCTTGGCTGTAAACAAGATGGAATGCTGTATCAGATTGAGTGGT 274  
Qy 785 AGCTGGGAGTGGGCTGTGTGCGCCCAATCGGCCCGGTGTCTACACAATATCAGCCAC 844  
Db 273 AGCTGGGAGTGGGCTGTGTGCGCCCAATCGGCCCGGTGTCTACACAATATCAGCCAC 214  
Qy 845 CACTTTGAGTGGATCCAGAGCTGATGGCCAGAGTGGCATGTCCAGCAGACACCCCTCC 904  
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Qy 905 TGGCCGCTACTCTTTTCCCTCTTCTGCGGCTCTCCCACTCTCTGGGCGGCTGTAGCC 964  
Db 153 TGGCCGCTACTCTTTTCCCTCTTCTGCGGCTCTCCCACTCTCTGGGCGGCTGTAGCC 94  
Qy 965 TACCTGAGCCCATGACAGCTGGGCGCACTGCCAAGTCAAGCCCTGGTCTTCTTCTT 1024
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Db	93	TACTGAGCCATGACACCTGGGGCCACTGCAAGTCAGGCCCTGGTCTCTCTGCTCTT 34
QY	1025	GTTTGGTAAATAACACATTCACGTTGATGC 1054
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RESULT 12		
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LOCUS		
DEFINITION	BM019026	705 bp mRNA linear EST 30-OCT-2001
ACCESSION	603647010F1 NIH_MGC_98	Homo sapiens cDNA clone IMAGE:5428539 5'
VERSION		mRNA sequence.
KEYWORDS	BM019026.1	GI:16533380
SOURCE		
ORGANISM		Homo sapiens (human)
REFERENCE		Homo sapiens
AUTHORS		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE		1 (bases 1 to 705)
JOURNAL		NIH-MGC http://mgc.nci.nih.gov/.
COMMENT		National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
		Contact: Robert Strausberg, Ph.D.
		Email: cgapbs-r@mail.nih.gov
		Tissue Procurement: ATCC
		cDNA Library Preparation: Ling Hong/Rubin Laboratory
		cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
		DNA Sequencing by: Incyte Genomics, Inc.
		Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
		http://image.llnl.gov
		Plate: L1CM1896 row: c column: 04
		High quality sequence start: 7
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		/lab_host="DH10B (phage-resistant)"
		/clone_lib="NIH_MGC_98"
		/notes="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
ORIGIN		
Query Match		51.7%; Score 569.2; DB 4; Length 705;
Best Local Similarity		93.1%; Pred. No. 4.3e-132;
Matches	650; Conservative	0; Mismatches 18; Indels 30; Gaps 4;
QY	27	GCGGGGCGCTGCTGCTGGCGCTGCTGCTGGCTGGGCTGGAAGCCGAGTCGC 86
Db	2	GCTGGGCGCTGCTGCTGGCGCTGCTGCTGGCTGGGCT-GACTCAGGAGCGCGAGTCGC 60
QY	87	AGGAGGGCGCGCTTATCAGGACCATGCGGCGACGGGTATCATCGTCGGCATTCGTGG 146
Db	61	A-GAGGCGGCGCGCTTATCAGGACCATGCGGCGCGAGCGGTATCATCGTCGGCATTCGTGG 119
QY	147	GTGAGAGGACGCCGAACCTCGGGCGTTGGCGCTGGGAGGGAGCGCTCGCTGTGGGATT 206
Db	120	GTGAGAGGACGCCGAACCTCGGGCGTTGGCGCTGGGAGGGAGCGCTCGCTGTGGGATT 179
QY	207	CCACGCTATCGGAGTGAGCTGCTGCTAGCCACCGCTGGGCACCTCACGGCGCGCACTGCT 266

cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN		FEATURES		
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		/lab_host="DH10B"		
		/clone_lib="NIH_MGC_119"		
		/notes="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH_MGC Library."		
ORIGIN		this is a NIH_MGC Library."		
Query Match		49.9%; Score 548.8; DB 4; Length 1219;		
Best Local Similarity	91.8%; Pred. No. 6.5e-127;			
Matches	602; Conservative 0; Mismatches 52; Indels 2; Gaps 2;			
Qy	106	AGGACCATCGCGCGGATCATCAGTCGCGGATTCGCCAGTATGCGGATGCGGAGTGA	165	
Db	111	AGGACCATCGCGCGGATCATCAGTCGCGGATTCGCCAGTATGCGGATGCGGAGTGA	170	
Qy	166	CGGCGGTTGGCC-GTGGCAGGGGAGCTGCGGATTCGCCAGTATGCGGATGCGGAGTGA	224	
Db	171	CGGCGGTTGGCC-GTGGCAGGGGAGCTGCGGATTCGCCAGTATGCGGATGCGGAGTGA	230	
Qy	225	GCCTGCTCAGCACCGCTGGGCACTACGCGGCGCACTGCTTTGAAACCTATAGTGACC	284	
Db	231	GCCTGCTCAGCACCGCTGGGCACTACGCGGCGCACTGCTTTGAAACCTATAGTGACC	290	
Qy	285	TTAGTGATCCCTCGGCGTGGATGTCAGTTGGCGGCTGACCTCCATGCGCATCTTCT	344	
Db	291	TTAGTGATCCCTCGGCGTGGATGTCAGTTGGCGGCTGACCTCCATGCGCATCTTCT	350	
Qy	345	GGAGCTCGAGCGCTACTACACCGTCTTCTGATCGAATATCTATCTAGCGCTCGCT	404	
Db	351	GGAGCTCGAGCGCTACTACACCGTCTTCTGATCGAATATCTATCTAGCGCTCGCT	410	
Qy	405	ACCTGGGGAATTCACCTTATGACATTCGCTTGGTGAAGCTGCTGCACTCTGACCTACA	464	
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Qy	465	CTAAACATCATCAGCGCATCTGCTCAGGCTCTCAATTTGAGTTGAGAACCGGACAG	524	
Db	471	CTAAACATCATCAGCGCATCTGCTCAGGCTCTCAATTTGAGTTGAGAACCGGACAG	530	
Qy	525	ACTGCTGGTCACTGGCTGGGGGTACATCAAGAGGATGAGGCACTGCACTCCCCACA	584	
Db	531	ACTGCTGGTCACTGGCTGGGGGTACATCAAGAGGATGAGGCACTGCACTCCCCACA	590	
Qy	585	CCCTCCAGGAATTCAGTCCGCTATCAAAACACTCTATGTGCAACCACTCTTCTCTCA	644	
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Qy	645	AGTACAGTTTCCGCAAGGACATCTTTGGAGAC 676		
Db	651	AGTACAGTTTCCGCAAGGACATCTCGGGAGAC 682		

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DEFINITION AGNCOURT 6558382 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5742958
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BM553333
VERSION BM553333.1 GI:18791973
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1219)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM12761 Row: O Column: 23
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ORIGIN		this is a NIH_MGC Library."	
Query Match		49.9%; Score 548.8; DB 4; Length 1219;	
Best Local Similarity	91.8%; Pred. No. 6.5e-127;		
Matches	602; Conservative 0; Mismatches 52; Indels 2; Gaps 2;		
Qy	106	AGGACCATCGCGCGGATCATCAGTCGCGGATTCGCCAGTATGCGGATGCGGAGTGA	165
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Qy	166	CGGCGGTTGGCC-GTGGCAGGGGAGCTGCGGATTCGCCAGTATGCGGATGCGGAGTGA	225
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Qy	226	CCCTGCTCAGCACCGCTGGGCACTACGCGGCGCACTGCTTTGAAACCTATAGTGACCT	285
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Qy	406	CCTGGGGAATTCACCTTATGACATTCGCTTGGTGAAGCTGCTGCACTGTCACTACAC	465
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Db	486	CTGCTGGGTGACTGGCTGGGGGTACATCAAGAGGATGAGGCACTGCCATCTCCCCACAC	545
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Db 666 CGCGGAGCGATGGCTGGCTTCCCGAGGGGCCCTTTGCGCAGCCACTCCAGGG 721

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DEFINITION
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sequence.
ACCESSION
AA161187
VERSION
AA161187.1 GI:1735441
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
AUTHORS
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Marlin, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trivasakis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R., and Marra, M.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 591)
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Marlin, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trivasakis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R., and Marra, M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478
889549
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40M13 fwd. from Amersham
High quality sequence stop: 386.
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ORIGIN

Query Match 47.8%; Score 525.8; DB 1; Length 591;
Best Local Similarity 97.0%; Pred. No. 3.5e-121;
Matches 574; Conservative 0; Mismatches 14; Indels 4; Gaps 4;

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Db 530 GTACATCAAGAGGATGAGGACATGCCATCTCCGACACCTCCAGGAAGTTCCAGGTCG 471
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Db 410 TCTTTGGAGACATGTTTGCTGGCAAAATGCCAAAGGCGGGAAGGATGCTGCTCGGT 351
Qy 725 GACTCAGGTGGACCCCTTGGCCTGTAAACAAGGATGGACTGTGGTATCAGATTGGAGTGGTG 784
Db 350 GACTCAGGTGGACCCCTTGGCCTGTAAACAAGATGGACTGTGGTATCAGATTGGAGTGGTG 291
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Qy 905 TGGCCGCTACTCTTTTTCCTCTTCTGCGGCTCTCCACTCTCTGGGGCCGGTCTGAGCC 964
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 5, 2005, 04:37:53 ; Search time 722.188 Seconds
(without alignments)
9038.138 Million cell updates/sec

Title: US-10-040-647-5

Perfect score: 1100

Sequence: 1 CGCGGAGAGAGGCCATGG.....AAAAAAAAAAAAAAAAAAAA 1100

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5401638 seqs, 2966923429 residues

Total number of hits satisfying chosen parameters: 10803276

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1100	100.0	1100	14	US-10-040-647-5
2	1090.6	99.1	1100	9	US-09-903-320-256
3	1090.6	99.1	1100	9	US-09-903-088B-256
4	1090.6	99.1	1100	9	US-09-905-291A-256
5	1090.6	99.1	1100	9	US-09-902-853-256
6	1090.6	99.1	1100	9	US-09-907-824-256
7	1090.6	99.1	1100	9	US-09-907-841-256
8	1090.6	99.1	1100	10	US-09-904-011-256
9	1090.6	99.1	1100	10	US-09-903-640-256
10	1090.6	99.1	1100	10	US-09-908-093-256
11	1090.6	99.1	1100	10	US-09-906-742-256

12 1090.6 99.1 1100 10 US-09-906-838-256 Sequence 256, App

13 1090.6 99.1 1100 10 US-09-907-613-256 Sequence 256, App

14 1090.6 99.1 1100 10 US-09-907-942-256 Sequence 256, App

15 1090.6 99.1 1100 10 US-09-904-859-256 Sequence 256, App

16 1090.6 99.1 1100 10 US-09-909-204-256 Sequence 256, App

17 1090.6 99.1 1100 10 US-09-904-820-256 Sequence 256, App

18 1090.6 99.1 1100 10 US-09-904-786-256 Sequence 256, App

19 1090.6 99.1 1100 10 US-09-906-646-256 Sequence 256, App

20 1090.6 99.1 1100 10 US-09-906-700-256 Sequence 256, App

21 1090.6 99.1 1100 10 US-09-903-786-256 Sequence 256, App

22 1090.6 99.1 1100 10 US-09-902-903-256 Sequence 256, App

23 1090.6 99.1 1100 10 US-09-903-749A-256 Sequence 256, App

24 1090.6 99.1 1100 10 US-09-904-119-256 Sequence 256, App

25 1090.6 99.1 1100 10 US-09-904-956-256 Sequence 256, App

26 1090.6 99.1 1100 10 US-09-902-736-256 Sequence 256, App

27 1090.6 99.1 1100 10 US-09-907-794-256 Sequence 256, App

28 1090.6 99.1 1100 10 US-09-903-943-256 Sequence 256, App

29 1090.6 99.1 1100 10 US-09-904-462-256 Sequence 256, App

30 1090.6 99.1 1100 10 US-09-907-925-256 Sequence 256, App

31 1090.6 99.1 1100 10 US-09-902-692-256 Sequence 256, App

32 1090.6 99.1 1100 10 US-09-903-520-256 Sequence 256, App

33 1090.6 99.1 1100 10 US-09-905-056-256 Sequence 256, App

34 1090.6 99.1 1100 10 US-09-909-064-256 Sequence 256, App

35 1090.6 99.1 1100 10 US-09-904-553-256 Sequence 256, App

36 1090.6 99.1 1100 10 US-09-905-381-256 Sequence 256, App

37 1090.6 99.1 1100 10 US-09-904-485-256 Sequence 256, App

38 1090.6 99.1 1100 10 US-09-905-348-256 Sequence 256, App

39 1090.6 99.1 1100 10 US-09-905-088-256 Sequence 256, App

40 1090.6 99.1 1100 10 US-09-907-575-256 Sequence 256, App

41 1090.6 99.1 1100 10 US-09-905-075-256 Sequence 256, App

42 1090.6 99.1 1100 10 US-09-902-759-256 Sequence 256, App

43 1090.6 99.1 1100 10 US-09-902-634-256 Sequence 256, App

44 1090.6 99.1 1100 10 US-09-902-713-256 Sequence 256, App

45 1090.6 99.1 1100 10 US-09-907-979-256 Sequence 256, App

ALIGNMENTS

RESULT 1

US-10-040-647-5
; Sequence 5, Application US/10040647
; Publication No. US20030092154A1
; GENERAL INFORMATION:
; APPLICANT: (US only) ANTALIS Toni Marie and HOOPER John David
; TITLE OF INVENTION: NOVEL MOLECULES
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/040.647
; FILING DATE: 07-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/023,942
; FILING DATE: <Unknown>
; APPLICATION NUMBER: POS101/97
; FILING DATE: 13-FEB-1997
; APPLICATION NUMBER: PP0422/97
; FILING DATE: 18-NOV-1997
; APPLICATION NUMBER: International PCT Application
; FILING DATE: 13-FEB-1998
; ATTORNEY/AGENT INFORMATION:


```

; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,291A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 256
; LENGTH: 1100
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-905-291A-256

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	Query Match	99.1%	Score 1090.6	DB 9	Length 1100	
	Best Local Similarity	99.6%	Pred. No. 0			
	Matches 1093	Conservative 0	Mismatches 4	Indels 0	Gaps 0	
Qy	1	CGCGGGAGAGGAGGCATGGCGCGCGGGGCGCTGCTGTGGCGCTGCTGTGGCTCG	60			
Db	4	CGCGGGAGAGGAGGCATGGCGCGCGGGGCGCTGCTGTGGCGCTGCTGTGGCTCG	63			
Qy	61	GGCTGGGACTCAGGAAGCCGGAGTGCAGGAGGGCGGCGCGTTATCAGGACCATGCGGCG	120			
Db	64	GGCTGGGACTCAGGAAGCCGGAGTGCAGGAGGGCGGCGCGTTATCAGGACCATGCGGCG	123			
Qy	121	ACGGGTCATCACGTCGCGCATCTGTGGGTGGAGAGACCGCGAACTCGGGCGGTGGCCCGT	180			
Db	124	ACGGGTCATCACGTCGCGCATCTGTGGGTGGAGAGACCGCGAATCTGGGGGTGGCCCGT	183			
Qy	181	GCAGGGAGCGCTGCGCCTGTGGGATTCCTCACTATGCGGAGTGAAGCTGCTCAGCCACG	240			
Db	184	GCAGGGAGCGCTGCGCCTGTGGGATTCCTCACTATGCGGAGTGAAGCTGCTCAGCCACG	243			

RESULT 5
US-09-902-853-256
; Sequence 256, Application US/09902853
; Publication No. US20020192659A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen

QY		241	CTGGGCACATCA CGGCGGCCG CAGTCTTTGA AACCTTAGTGACCTTAGTGATCCCTCCGG	300
Db		244	CTGGGCACATCA CGGCGGCCG CAGTCTTTGA AACCTTAGTGACCTTAGTGATCCCTCCGG	303
QY		301	GTGGATGGTCAGTTTGGCCAGCTGACTTCCATGCCCATTCTTCGAGCCTCGCAGGCCTA	360
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QY		361	CTACACCCGTTACTTCGTATCGAAATACTATCTGAGCCCTCGTACTCTGGGGAAATTCACC	420
Db		364	CTACACCCGTTACTTCGTATCGAAATACTATCTGAGCCCTCGTACTCTGGGGAAATTCACC	423
QY		421	CTATGACATTTGCTTCGTGTAAGCTGTCTCACCTGTCACTACACTAAACACATCCAGCC	480
Db		424	CTATGACATTTGCTTCGTGTAAGCTGTCTGCACTGTCACTACACTAAACACATCCAGCC	483
QY		481	CATCTGTCTCCAGGCCCTCCACATTTGAGTTTGAGAACCGGACAGACTGCTGGTGACTGG	540
Db		484	CATCTGTCTCCAGGCCCTCCACATTTGAGTTTGAGAACCGGACAGACTGCTGGTGACTGG	543
QY		541	CTGGGGGTACATCA AAGAGGATGAGCAGTCCATCTCCCCACACCCCTCCAGGAAGTTCA	600
Db		544	CTGGGGGTACATCA AAGAGGATGAGCAGTCCATCTCCCCACACCCCTCCAGGAAGTTCA	603
QY		601	GSTCGCCATCATAAA CAACCTATATGTGCAACCACTCTTCTCAA GTACAGTTTCGGCAA	660
Db		604	GSTCGCCATCATAAA CAACCTATATGTGCAACCACTCTTCTCAA GTACAGTTTCGGCAA	663
QY		661	GGACATCTTTGGAGACATGGTTTTGTGCTGGCAATGCCCAAGCGCGGAAGATGCCTGCTT	720
Db		664	GGACATCTTTGGAGACATGGTTTTGTGCTGGCAATGCCCAAGCGCGGAAGATGCCTGCTT	723
QY		721	CGGTGACTCAGGTGGACCTTTGGCCCTGTAAACAAGGATGACATGTGTGTATCAGATTGGAGT	780
Db		724	CGGTGACTCAGGTGGACCTTTGGCCCTGTAAACAAGGATGACATGTGTGTATCAGATTGGAGT	783
QY		781	CGTGAGCTGGGAGTGGGCTGTGGTCGGCCCAATCGCCCCGGTGTCTACACCAATATCAG	840
Db		784	CGTGAGCTGGGAGTGGGCTGTGGTCGGCCCAATCGCCCCGGTGTCTACACCAATATCAG	843
QY		841	CCACCACTTTGATGTGATCCAGAGCTGTATGSCCCAGAGTGGCATGTCCCGCCAGACCC	900
Db		844	CCACCACTTTGATGTGATCCAGAGCTGTATGSCCCAGAGTGGCATGTCCCGCCAGACCC	903
QY		901	CTCCTGGCCGCTACTCTTTTTCCCTCTCTGGGCTCTCCCACTCCTGGGGCCGGTCTG	960
Db		904	CTCCTGGCCGCTACTCTTTTTCCCTCTCTGGGCTCTCCCACTCCTGGGGCCGGTCTG	963
QY		961	AGCCTACCTGAGCCCATGAGCCTGGGGCCACTGCCAAGTCAAGGCCCTGGTTCTTCTCTG	1020
Db		964	AGCCTACCTGAGCCCATGAGCCTGGGGCCACTGCCAAGTCAAGGCCCTGGTTCTTCTCTG	1023
QY		1021	TCTTGTTCGTATAAACATTTCCAGTTTGATGCCCTTGACGGGCA TTTTTCAAAAAAA	1080
Db		1024	TCTTGTTCGTATAAACATTTCCAGTTTGATGCCCTTGACGGGCA TTTTTCAAAAAAA	1083
QY		1081	AAAAAAAAAAAAAAAA 1097	
Db		1084	AAAAAAAAAAAAAAAA 1100	

RESULT 5
US-09-902-853-256
; Sequence 256, Application US/09902853
; Publication No. US20020192859A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen

Db 784 CGTGAGCTGGGAGTGGGCTGTGGTGGCCCAATGGCCCGGCTGTCTACACCAATATCAG 843
Qy 841 CCACCACTTTGAGTGGATCCAGAAGCTGATGGCCCAAGAGTGGCATGTCCAGCCAGACCC 900
Db 844 CCACCACTTTGAGTGGATCCAGAAGCTGATGGCCCAAGAGTGGCATGTCCAGCCAGACCC 903
Qy 901 CTCCTGGCCGCTACTCTCTTTTCCCTCTCTCTCTGGGCTCTCCCACTCTCTGGGCGGCTGTG 960
Db 904 CTCCTGGCCGCTACTCTCTTTTCCCTCTCTCTCTGGGCTCTCCCACTCTCTGGGCGGCTGTG 963
Qy 961 AGCTACTCTAGCCCACTGAGCCCTGGGGCCACTGGCCCAAGTCAAGCCCTGGTCTCTCTCTG 1020
Db 964 AGCTACTCTAGCCCACTGAGCCCTGGGGCCACTGGCCCAAGTCAAGCCCTGGTCTCTCTCTG 1023
Qy 1021 TCTGTTTGGTAAATAAACACATTCAGTTCAGTTCGATGCTTGCAGGGCATTTTTCAAAAAAAA 1080
Db 1024 TCTGTTTGGTAAATAAACACATTCAGTTCAGTTCGATGCTTGCAGGGCATTTCTCAAAAAAAA 1083
Qy 1081 AAAAAAAAAAAAAA 1097
Db 1084 AAAAAAAAAAAAAA 1100

RESULT 9
US-09-903-640-256
; Sequence 256, Application US/09903640
; Publication No. US20030017463A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/903,640
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 256
; LENGTH: 1100
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-903-640-256

Query Match 99.1%; Score 1090.6; DB 10; Length 1100;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1093; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGGGGAGAGGAGCCATGGGCGCGCGCGCGCGCGCTGTCTGTGGCGCTGTCTGTGGCTCG 63
Qy 61 GGCTGGACTCAGGAAGCCGAGTTCGAGAGGCGCGCGCGCTGTATCAGGACCATGCGGCGG 120
Db 64 GGCTGGACTCAGGAAGCCGAGTTCGAGAGGCGCGCGCGCTGTATCAGGACCATGCGGCGG 123
Qy 121 ACGGCTCATCAGTTCGCGCATCTGTGGTGGAGAGGACGCCGAACCTCGGCGGTGGCCGTG 180
Db 124 ACGGCTCATCAGTTCGCGCATCTGTGGTGGAGAGGAGCGCGGAACCTCGGCGGTGGCCGTG 183
Qy 181 GCAGGGAGGCGCTGGCGCTGTGGATTCACACGATATGCGAGTGGAGCTCTCAGCCACCG 240
Db 184 GCAGGGAGGCGCTGGCGCTGTGGATTCACACGATATGCGAGTGGAGCTCTCAGCCACCG 243
Qy 241 CTGGGCACTCAGCGCGCGCGCATCTGCTTTGAAAACCTATAGTACCTTTAGTGATCCCTCCG 300
Db 244 CTGGGCACTCAGCGCGCGCGCATCTGCTTTGAAAACCTATAGTACCTTTAGTGATCCCTCCG 303
Qy 301 GTGGATGGTCCAGTTCGCGCATCTGATTCATTCATTCATTCATTCATTCATTCATTCATTC 360
Db 304 GTGGATGGTCCAGTTCGCGCATCTGATTCATTCATTCATTCATTCATTCATTCATTCATTC 363
Qy 361 CTACACCGCTTACTTGGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGAAATTCACC 420
Db 364 CTACACCGCTTACTTGGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGAAATTCACC 423
Qy 421 CTATGACATTCGCTTGGTCAAGCTGTCTGACCTGTCTGACCTACACTAAACACATCCAGCC 480
Db 424 CTATGACATTCGCTTGGTCAAGCTGTCTGACCTGTCTGACCTACACTAAACACATCCAGCC 483
Qy 481 CATCTGTCTCCAGGCGCTCCACATTTGAGTTTGAGAACCGGACAGACTGTCTGGTGACTGG 540
Db 484 CATCTGTCTCCAGGCGCTCCACATTTGAGTTTGAGAACCGGACAGACTGTCTGGTGACTGG 543
Qy 541 CTGGGGGTACATCAAGAGGATGAGGCACTGCATCTCCCAACCTCCAGCCCTCCAGGAAATTC 600
Db 544 CTGGGGGTACATCAAGAGGATGAGGCACTGCATCTCCCAACCTCCAGCCCTCCAGGAAATTC 603
Qy 601 CGTGGCGCATATAAACCAACTCTATGTGCAACCACTCTTCCTCAAGTACAGTTTCGCA 660
Db 604 GGTGGCGCATATAAACCAACTCTATGTGCAACCACTCTTCCTCAAGTACAGTTTCGCA 663
Qy 661 GGACATCTTTGGAGACATGGTTTGTGTGGCAATGCCAAGCGGGAAGGATGCCTGCTT 720
Db 664 GGACATCTTTGGAGACATGGTTTGTGTGGCAATGCCAAGCGGGAAGGATGCCTGCTT 723
Qy 721 CGGTGACTCAGGTGGACCCCTTGGCTGTAAACAGGATGAGCTGTGTATCAGATTGGAGT 780
Db 724 CGGTGACTCAGGTGGACCCCTTGGCTGTAAACAGGATGAGCTGTGTATCAGATTGGAGT 783
Qy 781 CGTGAGCTGGGAGTGGGCTGTGGTGGCCCAATCGGCGCGGCTGTCTACACCAATATCAG 840
Db 784 CGTGAGCTGGGAGTGGGCTGTGGTGGCCCAATCGGCGCGGCTGTCTACACCAATATCAG 843
Qy 841 CCACCACTTTGAGTGGATCCAGAAGCTGATGGCCCAAGAGTGGCATGTCCAGCCAGACCC 900
Db 844 CCACCACTTTGAGTGGATCCAGAAGCTGATGGCCCAAGAGTGGCATGTCCAGCCAGACCC 903
Qy 901 CTCCTGGCGCTACTCTTTTCCCTCTCTCTGGGCTCTCCCACTCTCTGGGCGGCTGTG 960
Db 904 CTCCTGGCGCTACTCTTTTCCCTCTCTCTGGGCTCTCCCACTCTCTGGGCGGCTGTG 963
Qy 961 AGCTACTCTAGCCCACTGAGCCCTGGGGCCACTGGCCCAAGTCAAGCCCTGGTCTCTCTCTG 1020
Db 964 AGCTACTCTAGCCCACTGAGCCCTGGGGCCACTGGCCCAAGTCAAGCCCTGGTCTCTCTCTG 1023
Qy 1021 TCTGTTTGGTAAATAAACACATTCAGTTCAGTTCGATGCTTGCAGGGCATTTTTCAAAAAAAA 1080
Db 1024 TCTGTTTGGTAAATAAACACATTCAGTTCAGTTCGATGCTTGCAGGGCATTTCTCAAAAAAAA 1083
Qy 1081 AAAAAAAAAAAAAA 1097
Db 1084 AAAAAAAAAAAAAA 1100


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QY 541 CTGGGGTACATCAAGAGGATGAGGCACTCCCATCTCCCCACACCCCTCCAGGAAGTCA 600
Db 544 CTGGGGGTACATCAAGAGGATGAGGCACTCCCATCTCCCCACACCCCTCCAGGAAGTCA 603
QY 601 GGTGCCATCAATCAACTCTATGTGCAACACCTCTTCTCAAGTACAGTTTCGCCAA 660
Db 604 GGTGCCATCAATCAACTCTATGTGCAACACCTCTTCTCAAGTACAGTTTCGCCAA 663
QY 661 GGACATCTTTGGAGACATGGTTTGTCTGGCAATGCCCAAGCGGGAAGATGCTGCTT 720
Db 664 GGACATCTTTGGAGACATGGTTTGTCTGGCAACGCCCAAGCGGGAAGATGCTGCTT 723
QY 721 CGGTGACTCAGGTGACCCCTTGGCCCTGTAAACAAGATGAGCTGTGGTATCAGATTGGAGT 780
Db 724 CGGTGACTCAGGTGACCCCTTGGCCCTGTAAACAAGATGAGCTGTGGTATCAGATTGGAGT 783
QY 781 CGTGAGCTGGGAGTGGGCTGTGTGGCCCAATCGGCCCGCTCTACACCAATATCAG 840
Db 784 CGTGAGCTGGGAGTGGGCTGTGTGGCCCAATCGGCCCGCTCTACACCAATATCAG 843
QY 841 CCACCATTTGAGTGGATCCAGAAAGCTGATGGCCAGAGTGGCATGTCCAGCCAGACCC 900
Db 844 CCACCATTTGAGTGGATCCAGAAAGCTGATGGCCAGAGTGGCATGTCCAGCCAGACCC 903
QY 901 CTCCTGGCCGTACTCTTTTCCCTCTTCTCTGGGCTCTCCACTCTCTGGGGCCGGTCTG 960
Db 904 CTCCTGGCCGTACTCTTTTCCCTCTTCTCTGGGCTCTCCACTCTCTGGGGCCGGTCTG 963
QY 961 AGCTTACTGAGCCATGCAGCCCTGGGGCCACTGCCAAGTCAGGCCCTGTTCTCTCTG 1020
Db 964 AGCTTACTGAGCCATGCAGCCCTGGGGCCACTGCCAAGTCAGGCCCTGTTCTCTCTG 1023
QY 1021 TCTTGTGGTAAATAACACATTCAGTTGATGCTTGCGGGCATTTTCAAAAAAAA 1080
Db 1024 TCTTGTGGTAAATAACACATTCAGTTGATGCTTGCGGGCATTTTCAAAAAAAA 1083
QY 1081 AAAAAA 1097
Db 1084 AAAAAA 1100
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RESULT 13

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US-09-907-613-256
; Sequence 256, Application US/0907613
; Publication No. US20030027145A1
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GENERAL INFORMATION:

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; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
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; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,613
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
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; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
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; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 256
; LENGTH: 1100
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-907-613-256
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Query Match 99.1%; Score 1090.6; DB 10; Length 1100;

Best Local Similarity 99.6%; Pred. No. 0;

Matches 1093; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY 1 CGCGGAGAGGAGGCCATGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 60
Db 4 CGCGGAGAGGAGGCCATGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 63
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QY 361 CTACACCGGTACTTCTGTATCGAATATCTATCTGAGCCCTCGTACTCTGGGGAATTCACC 420
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Db 1084 AAAAAAAAAAAAAA 1100

Search completed: March 5, 2005, 15:38:10
Job time : 727.188 secs

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121 ACGGGTCTATCAGTCCGCGCATCGTGGTGGAGAGAGAGCGCGAACTCGGGCGTTGGCGGTG 180
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181 GCAGGGAGCGCTCGCGCTGTCGGGATCCACGATGCGGAGTGGAGCTGCTCAGCCACCG 240
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241 CTGGGCACTCAGCGGGCGCACTGCTTTGAAACCTATAGTGACCTTAGTGATCCCTCCGG 300
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364 CTACACCGTTTACTTCTGATCGAATATCTATCTGAGCCCTCGCTACCTGGGGAAATTCACC 423
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901 CTCCTGGCGCTACTCTTTTTCCTTCTCTCTGCGCTCTCCACTCTCTGGGGCGGCTCG 960
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 4, 2005, 22:18:30 ; Search time 205.888 Seconds
(without alignments)
8742.154 Million cell updates/sec

Title: US-10-040-647-5

Perfect score: 1100

Sequence: 1 CGCGGGAGAGGCGCATGG.....AAAAAAAAAAAAAAAAAAAA 1100

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents NA.*
- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1090.6	99.1	1100	4	US-09-905-125A-256
4	1090.6	99.1	1100	4	US-09-902-775A-256
5	1090.6	99.1	1100	4	US-09-906-700-256
6	1090.6	99.1	1100	4	US-09-903-603A-256
7	1090.6	99.1	1100	4	US-09-904-920A-256
8	1090.6	99.1	1100	4	US-09-909-064-256
9	1090.6	99.1	1100	4	US-09-905-381A-256
10	1090.6	99.1	1100	4	US-09-906-618-256
11	1078	98.0	1094	4	US-09-023-942A-3
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13	751	68.3	1103	3	US-09-386-642-59
14	482.2	43.8	959	4	US-09-023-942A-25
15	351.6	32.0	3866	4	US-09-023-942A-27
16	168.2	15.3	1110	3	US-09-386-653A-1
17	165	15.0	1212	4	US-09-620-312D-431
18	164.8	15.0	980	4	US-09-023-942A-30
19	157.4	14.3	1130	3	US-09-386-653A-8
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22	133	12.1	1378	4	US-09-905-125A-262
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28	133	12.1	1378	4	US-09-905-381A-262	Sequence 262, App
29	133	12.1	1378	4	US-09-906-618-262	Sequence 262, App
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31	128.4	11.7	1166	3	US-09-386-629-2	Sequence 2, Appli
32	125.8	11.4	942	4	US-09-636-382A-3	Sequence 3, Appli
33	119.6	10.9	2440	4	US-09-949-016-5210	Sequence 5210, Ap
34	119.6	10.9	2440	4	US-09-949-016-5211	Sequence 5211, Ap
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38	117	10.6	1108	2	US-09-016-366A-14	Sequence 14, Appl
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40	115.4	10.5	1137	2	US-09-016-366A-18	Sequence 18, Appl
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44	114.8	10.4	1748	4	US-09-879-792-11	Sequence 11, Appl
45	114	10.4	1615	4	US-09-820-002-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
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; Sequence 5, Application US/09023942A
; Patent No. 6479274
; GENERAL INFORMATION:
; APPLICANT: (US only) ANTALIS Toni Marie and HOOPER John David
; TITLE OF INVENTION: NOVEL MOLECULES
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,942A
; FILING DATE: 13-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: POS101/97
; FILING DATE: 13-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PP0422/97
; FILING DATE: 18-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: International PCT Application
; FILING DATE: 13-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: DIGIGLIO, FRANK S
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 11169
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742 4343
; TELEFAX: (516) 742 4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1100 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: CDS

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DB 904 CTCCTGGCGGTACTCTTTTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 963
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DB 1024 TCTTGTGGTAAATAAACAACATTCAGTTGATGCTTGCAGGGGATTTTCAAAAAA 1083
QY 1081 AAAAAA 1097
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RESULT 10

US-09-606-618-256
; Sequence 256, Application US/0906618
; Patent No. 6828146
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906.618
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13

; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
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; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 256
; LENGTH: 1100
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-606-618-256

Query Match 99.1%; Score 1090.6; DB 4; Length 1100;

Best Local Similarity 99.6%; Pred. No. 2.7e-232;

Matches 1093; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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DB 544 CTGGGGGTACATCAAGAGGATGAGGACCTGCCATCTCTCCACACCTCTCAGGAGGTTCA 603

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Db 784 CGTGAGCTGGGAGTGGCTGTGTGGCCCAATCGGCCCGGTCTTACACCAATATCAG 843
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QY 1081 AAAAAAAAAAAAAAAAAA 1097
Db 1084 AAAAAAAAAAAAAAAAAA 1100

RESULT 11
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; Sequence 3, Application US/09023942A
; Patent No. 6479274
; GENERAL INFORMATION:
; APPLICANT: (US only) ANTALIS Toni Marie and HOOPER John David
; TITLE OF INVENTION: NOVEL MOLECULES
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,942A
; FILING DATE: 13-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: POS101/97
; FILING DATE: 13-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PP0422/97
; FILING DATE: 18-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: International PCT Application
; FILING DATE: 13-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: DIGIGLIO, FRANK S
; REGISTRATION NUMBER: 31,346
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; REFERENCE/DOCKET NUMBER: 11168
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742 4343
; TELEFAX: (516) 742 4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1094 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 17..955
; US-09-023-942A-3

Query Match 98.0%; Score 1078; DB 4; Length 1094;
Best Local Similarity 99.5%; Pred. No. 8.3e-289;
Matches 1094; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

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Db 295 GTGGATGGTCCAGTTTGGCCAGCTGACTTCATGCCATCTCTCTGAGGCTGAGGCGCTA 354
QY 361 CTACACCGTTACTTCGTATCGAATATCTATCTGAGCCTCGCTACTCTGGGGAATTCACC 420
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Db 984 AGCTACCTGAGCCCATGACGCTGGGGCCACTGCCAAGTCAGGCCCTGCTTCTTCTG 1043
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; Sequence 59, Application US/09386642
; Patent No. 6420157
; GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew
; APPLICANT: Qi, Jensen
; APPLICANT: Andrade-Gordon, Patricia
; TITLE OF INVENTION: Zymogen Activation System
; FILE REFERENCE: ORT-1028
; CURRENT APPLICATION NUMBER: US/09/386,642
; CURRENT FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 59
; LENGTH: 1103
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic acid
; OTHER INFORMATION: sequence of human protease F in CPEK2 zymogen
; OTHER INFORMATION: vector
US-09-386-642-59
Query Match 68.3%; Score 751; DB 3; Length 1103;
Best Local Similarity 93.4%; Pred. No. 4.4e-198;
Matches 784; Conservative 0; Mismatches 55; Indels 0; Gaps 0;
Qy 140 ATCTGGGTGAGAGGAGCGGAACCTCGGGCTGGTGGCAGGGAGCCCTGCGCTG 199
Db 139 ATCTGGGGGCTATGCTCTAGAACTCGGGCTGGTGGCAGGGAGGCGCTGCGCTG 198
Qy 200 TGGGATTCACAGTATCGGGATGAGCTGCTAGCCACCGCTGGGCACTCAGCGGGCG 259
Db 199 TGGGATTCACAGTATCGGGATGAGCTGCTAGCCACCGCTGGGCACTCAGCGGGCG 258
Qy 260 CACTGCTTTGAAACTATAGTACCTTAGTATCCCTCGGGTGGATGCTCCAGTTGGC 319
Db 259 CACTGCTTTGAAACTATAGTACCTTAGTATCCCTCGGGTGGATGCTCCAGTTGGC 318
Qy 320 CAGCTGACTTCCATGCCATCCTCTGAGCCTGAGCGCTGAGCGCTACTACAACCGTTACTTGGTA 379
Db 319 CAGCTGACTTCCATGCCATCCTCTGAGCCTGAGCGCTGAGCGCTACTACAACCGTTACTTGGTA 378
Qy 380 TCGAATATCTAGACCCCTCGTACTCGGGGAATTCACCTATGACATTCCTTGGTG 439
Db 379 TCGAATATCTAGACCCCTCGTACTCGGGGAATTCACCTATGACATTCCTTGGTG 438
Qy 440 AAGCTGTCTGACCTGTCACTACATAAACAATCCAGCCCACTGTCTCCAGGCGCTCC 499
Db 439 AAGCTGTCTGACCTGTCACTACATAAACAATCCAGCCCACTGTCTCTCCAGGCGCTCC 498
Qy 500 ACATTGAGTTTGAGAACCGGACAGACTGTGGTGTGACTGGCTGGGGGTACATCAAGAG 559
Db 499 ACATTGAGTTTGAGAACCGGACAGACTGTGGTGTGACTGGCTGGGGGTACATCAAGAG 558
Qy 560 GATGAGGACTGCCATCTCCCAACCCCTCCAGAGTTTCAGGTCGCATCATTAACAAC 619
Db 559 GATGAGGACTGCCATCTCCCAACCCCTCCAGAGTTTCAGGTCGCATCATTAACAAC 618
Qy 620 TCTATGTCAACACCTCTTCTCAAGTACAGATTTCCGCAAGGACATCTTTGGAGACATG 679
Db 619 TCTATGTCAACACCTCTTCTCAAGTACAGATTTCCGCAAGGACATCTTTGGAGACATG 678
Qy 680 GTTGTGCTGGCAATGCCCAGGCGGAGAGATGCTGCTTGGTGTACTCAGGTGGACCC 739

Db 679 GTTGTGCTGGCAATGCCAAGCGGGAAGATGCTGCTTGGTGTACTCAGGTGGACCC 738
Qy 740 TTGGCCCTGTAAACAAGATGAGCTGTGTATCAGATTGGAGTCTGAGCTGGGAGTGGGC 799
Db 739 TTGGCCCTGTAAACAAGATGAGCTGTGTATCAGATTGGAGTCTGAGCTGGGAGTGGGC 798
Qy 800 TGTGCTGGGCCCAATCGGCCCGGTGTCTACCAATATCAGCCACCACTTTGAGTGGATC 859
Db 799 TGTGCTGGGCCCAATCGGCCCGGTGTCTACCAATATCAGCCACCACTTTGAGTGGATC 858
Qy 860 CAGAAGCTGATGCCCCAGAGTGGCATGTCCAGCCAGACCCCTCTCGGCCGCTACTCTTT 919
Db 859 CAGAAGCTGATGCCCCAGAGTGGCATGTCCAGCCAGACCCCTCTCTGCTGACATCAC 918
Qy 920 TTCCCTCTTCTCTGGGCTCTCCACCTCTGGGGCGGTCTGAGCCTACCTGAGCCCATG 978
Db 919 CATCACATCCTAGCGGCCGCTTCCCTTTAGTGAGGGTTAATGCTTCGAGCAGACATG 977
RESULT 14
US-09-023-942A-25
; Sequence 25, Application US/09023942A
; Patent No. 6479274
; GENERAL INFORMATION:
; APPLICANT: (US only) ANTALIS Toni Marie and HOOPER John David
; TITLE OF INVENTION: NOVEL MOLECULES
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULDY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,942A
; FILING DATE: 13-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: P05101/97
; FILING DATE: 13-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: P0422/97
; FILING DATE: 18-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: International PCT Application
; FILING DATE: 13-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: DIGILIO, FRANK S
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 11168
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742 4343
; TELEFAX: (516) 742 4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 959 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2..856
US-09-023-942A-25

Query Match

43.8%; Score 482.2; DB 4; Length 959;

Best Local Similarity 71.3%; Pred. No. 1.5e-123; Mismatches 253; Indels 18; Gaps 2; Matches 672; Conservative 0;

101 TTATCAGGACCATCGGCGGACGCGGTTCATCAGCTGGCGATCGTGGGTGGAGAGAGCGCC 160
Db 8 TTGTGAGGCGGCTGGGTTCAGGACCATCCCTTCCGCTATAGTGGGTGGGATGATGCT 67

161 GAACTCGGCGGCTGGCGGTGGAGAGCGCTGGCGCTGTGGGATGCCAGATAGCGGA 220
Db 68 GAGCTTGGCGGCTGGCGGTGGAGAGCGCTGGCGCTGTGGGATGCCAGATAGCGG 127

221 GTGAGCGCTGCTCAGCCCGCTGGGCACTCAGCGGGCGGCACTGCTTTGAAACCTATAGT 280
Db 128 GCAACCTTGTCTCAACCGCGCTGGGTGCTTACAGTGCCTCCACTGCTTCCAAA----- 179

281 GACCTTAGTATCCCTCGGCTGGATGCTTCCAGTTTGGCCAGCTGACTTCCATGCCATCC 340
Db 180 -AGATAACGATCTTTTGTAGCTGGACGATCAGTTTGGTGGCTGACTTCCAGCGCATCT 238

341 TTCTGGAGCGCTGAGGCGCTACTACACCGGTTACTTCTGATCGAATATCTATCTGAGCGCT 400
Db 239 CTCTGGAACTTACAGGCGCTATTCGAACCGTTTACCAAAATAGAAATATTTTCTGAGCGCC 298

401 CGCTACCTGGGGAATTCACCTATGATTCGCTTGGTGGAGCTGCTGCACCTGTCAAC 460
Db 299 AAGTACTCGGAGAGATTCCTCAATGACATAGCCCTGCTGAGCTGTCTATCTCCAGTCACC 358

461 TACATAAACAATCCAGCCCATCTGCTCCAGCGCTCCACATTTGAGTTTGAGAACCGG 520
Db 359 TACATAATCTTATCCAGCCCATCTGCTTCTGACTCCAGTACAGTTTGAAGACCGA 418

521 ACAGACTGCTGGGTGACTGCTGGGGTACATCAAGAGGATGAGGCACTGCCATCTCCC 580
Db 419 ACTGACTGCTGGGTGACTGCTGGGGTACATCAAGAGGATGAGGCTGCTGCCATCTCCC 478

581 CAGACCTCCAGGAGTTTCAAGTCCGCTCATCAAACTATGTTGCAACCACTCTTC 640
Db 479 AACACTCTCCAGGAGTGCAGGTAGCTATTTATCAACCAAGAGTGTGTAAACCATATGATC 538

641 CTCAAGTACAGTTTCCGCAAGGACATCTTTGGAGACATGTTTGTGCTGGCAATGCCAA 700
Db 539 AAAAGCCAGACTTCCGCAAGGACATCTTTGGAGACATGTTTGTGCTGGCAATGCCAA 598

701 GCGGGAAGGATGCTGCTGCTGGGTGACTCAGGTGGACCTTTGGCTGTAAAGGATGGA 760
Db 599 GGTGCAAGGATGCTGCTGCTGGGTGACTCAGGTGGACCTTTGGCTGTAAAGGATGGA 658

761 CTGTGATCAGATGAGTGGAGTGGGAGTGGGCTGTGCTGGGCTGCTGCTGGGCTTCC 820
Db 659 GTGTGATCAGATGAGTGGAGTGGGAGTGGGCTGTGCTGGGCTGCTGCTGGGCTTCC 718

821 GGTGCTTACACCAATATCAGCCACACATTTTGGAGTGGATCCAGAGCTGATGGCCACAGT 880
Db 719 GGAGTCTATACCAATCAGTATCATCACTGATGATCCAGTCAACCATGATCCGCAAT 778

881 GGCAATGCTCCAGCAGACCCCTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 940
Db 779 GGGCTGCTCAGGCTGAGCCAGTCCCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 838

941 CCATCTCTGGGCGGCTGAGCTGCTGAGCCCATGAGCCCATGAGCCCTGAGCCCATGAGT 1000
Db 839 TCTTGTGCTGAGGCTGCTGAGCCCATGAGCCCATGAGCCCATGAGCCCATGAGT 889

1001 CAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1043
Db 890 CAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 932

RESULT 15

US-09-023-942A-27

; Sequence 27, Application US/09023942A

; Patent No. 6479274

; GENERAL INFORMATION:

APPLICANT: (US only) ANTHALIS Toni Marie and HOOPER John David
TITLE OF INVENTION: NOVEL MOLECULES
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 GARDEN CITY PLAZA
CITY: GARDEN CITY
STATE: NEW YORK
COUNTRY: USA
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,942A
FILING DATE: 13-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: POS101/97
FILING DATE: 13-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP0422/97
FILING DATE: 18-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: International PCT Application
FILING DATE: 13-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: DIGILIO, FRANK S
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 11168
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742 4343
TELEFAX: (516) 742 4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 3866 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-023-942A-27

Query Match 32.0%; Score 351.6; DB 4; Length 3866;
Best Local Similarity 97.5%; Pred. No. 5.3e-87;
Matches 357; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 710 GATGCTCTGCTTCGGTGAATCAGGTGGACCTTGGCTGTAAAGGATGAGTGTGAT 769
Db 3336 GCTGCTCCCGAGGTGACTCAGGTGGACCTTGGCTGTAAAGGATGAGTGTGAT 3395

Qy 770 CAGATTGGAGTCTGAGCTGGGAGTGGGCTGTGGCCCAATCGGCCGGTGTCTAC 829
Db 3396 CAGATTGGAGTCTGAGCTGGGAGTGGGCTGTGGCCCAATCGGCCGGTGTCTAC 3455

Qy 830 ACCAATATCAGCCACCATTTTGGATGATCCAGAGCTGATGGCCAGAGTGGCATGTCC 889
Db 3456 ACCAATATCAGCCACCATTTTGGATGATCCAGAGCTGATGGCCAGAGTGGCATGTCC 3515

Qy 890 CAGCCAGACCCCTCTGCGGCTACTCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCT 949
Db 3516 CAGCCAGACCCCTCTGCGGCTACTCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCT 3575

Qy 950 GGGCGGCTCTGAGCTTACCTGAGCCCATGAGCCCTGGGGCCATGCGCAAGTCAGGCCCTG 1009
Db 3576 GGGCGGCTCTGAGCTTACCTGAGCCCATGAGCCCTGGGGCCATGCGCAAGTCAGGCCCTG 3635

Qy 1010 GTTCT 1069
Db 3636 GTTCT 3695

Qy 1070 TCAAAA 1075
| | | | |
Db 3696 TCAAAA 3701

Search completed: March 5, 2005, 09:20:35
Job time : 209.888 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 4, 2005, 20:46:39 ; Search time 674.27 Seconds
(without alignments)
9657.430 Million cell updates/sec

Title: US-10-040-647-5

Perfect score: 1100

Sequence: 1 CGCGGAGAGAGGCCATGG.....AAAAAAAAAAAAAAAAAAAA 1100

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_16Dec04.*

1: Geneseqn1980s.*

2: Geneseqn1990s.*

3: Geneseqn2000s.*

4: Geneseqn2001as.*

5: Geneseqn2001bs.*

6: Geneseqn2002as.*

7: Geneseqn2002bs.*

8: Geneseqn2003as.*

9: Geneseqn2003bs.*

10: Geneseqn2003cs.*

11: Geneseqn2003ds.*

12: Geneseqn2004as.*

13: Geneseqn2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1098.4	99.9	1100	2	AAV59119 Nucleotid
2	1090.6	99.1	1100	2	AAV59119 Protein P
3	1090.6	99.1	1100	3	AAV59119 Human PRO
4	1090.6	99.1	1100	4	AAV59119 Human PRO
5	1090.6	99.1	1100	8	AAV59119 Human CDN
6	1090.6	99.1	1100	8	AAV59119 Novel hum
7	1090.6	99.1	1100	8	AAV59119 Human CDN
8	1090.6	99.1	1100	8	AAV59119 Human sec
9	1090.6	99.1	1100	8	AAV59119 Human sec
10	1090.6	99.1	1100	8	AAV59119 Human sec
11	1090.6	99.1	1100	8	AAV59119 Human sec
12	1090.6	99.1	1100	8	AAV59119 Human sec
13	1090.6	99.1	1100	9	AAV59119 Human sec
14	1090.6	99.1	1100	9	AAV59119 Human sec
15	1090.6	99.1	1100	9	AAV59119 Human sec
16	1090.6	99.1	1100	9	AAV59119 Human CDN
17	1090.6	99.1	1100	9	AAV59119 Human PRO
18	1090.6	99.1	1100	9	AAV59119 Human PRO
19	1090.6	99.1	1100	9	AAV59119 Human sec
20	1090.6	99.1	1100	9	AAV59119 Human PRO

21	1090.6	99.1	1100	9	ADA16716	ADA16716 Human sec
22	1090.6	99.1	1100	9	ADA13145	ADA13145 Human sec
23	1090.6	99.1	1100	9	ADA42013	ADA42013 Human sec
24	1090.6	99.1	1100	9	ADA17360	ADA17360 Human sec
25	1090.6	99.1	1100	9	ADA42863	ADA42863 Human sec
26	1090.6	99.1	1100	9	ACD23702	ACD23702 Human PRO
27	1090.6	99.1	1100	10	ADB77782	ADB77782 Human sec
28	1090.6	99.1	1100	10	ADB74918	ADB74918 Human sec
29	1090.6	99.1	1100	10	ADC28564	ADC28564 Human sec
30	1090.6	99.1	1100	10	ADC39764	ADC39764 Human sec
31	1090.6	99.1	1100	10	ADC40278	ADC40278 Human sec
32	1090.6	99.1	1100	10	ADC19102	ADC19102 Human sec
33	1090.6	99.1	1100	10	ADC34402	ADC34402 Human sec
34	1090.6	99.1	1100	10	ADC29457	ADC29457 Human sec
35	1090.6	99.1	1100	10	ADC28988	ADC28988 Human sec
36	1090.6	99.1	1100	10	ADC40873	ADC40873 Human sec
37	1090.6	99.1	1100	10	ADC19530	ADC19530 Human sec
38	1090.6	99.1	1100	10	ADC33978	ADC33978 Human sec
39	1090.6	99.1	1100	10	ADC13048	ADC13048 Human sec
40	1090.6	99.1	1100	10	ADC12500	ADC12500 Human sec
41	1090.6	99.1	1100	10	ADD05055	ADD05055 Human sec
42	1090.6	99.1	1100	10	ADD04061	ADD04061 Human sec
43	1090.6	99.1	1100	10	ADD03637	ADD03637 Human sec
44	1090.6	99.1	1100	10	ADE34889	ADE34889 Human sec
45	1090.6	99.1	1100	10	ADD89044	ADD89044 Encoding

ALIGNMENTS

RESULT 1	
AAV59119	
ID	AAV59119 standard; DNA; 1100 BP.
AC	AAV59119;
XX	
DT	07-JAN-1999 (first entry)
XX	
DE	Nucleotide sequence of long isoform of HELA2.
XX	
KW	Serine protease; regulation; cell activity; viability; HELA2; ATC2;
KW	BCOM3; testisin; fertility; suppressor; testicular germ cell cancer;
KW	seminoma; testis-specific expression; antitumour; sperm development;
KW	infertility; ss.
XX	
OS	Homo sapiens.
XX	
FT	Key
CDS	Location/Qualifiers
FT	17..961
FT	/*tag= a
FT	/product= "HELA2"
XX	
PN	W09836054-A1.
XX	
PD	20-AUG-1998.
XX	
PF	13-FEB-1998; 98WO-AU0000085.
XX	
PR	13-FEB-1997; 97AU-00005101.
PR	18-NOV-1997; 97AU-00000422.
XX	
PA	(AMRA-) AMRAD OPERATIONS PTY LTD.
XX	
PI	Antalis TM, Hooper JD;
XX	
DR	WPI; 1998-480768/41.
DR	P-ESDB; AAW77297.
XX	
PT	New serine protease(s) and kinase involved in regulating cell activity
PT	and viability - particularly the testis-specific protease HELA2 used for
XX	modulation of fertility and as tumour suppressor.
PS	Claim 6; Page 62-64; 167pp; English.

XX CC The present sequence represents the nucleotide sequence of the long
CC isoform of HELA2. cDNA generated from HeLa cells and PAI-2 expressing
CC HeLa cells was amplified using PCR primers AAV48312-13. Three new
CC sequences were detected in the 480 bp amplicon. These sequences are
CC designated HELA2 and AXC2 which have high homology to serine proteases
CC and BCOM3 which has homology to a kinase. The proteins are involved in or
CC associated with regulation of cell activity and/or viability.
CC Administration of recombinant HELA2 (also called testisin) is used to
CC increase fertility. Downregulation of HELA2 reduces fertility. HELA2 is
CC also a suppressor of testicular germ cell cancers (seminoma) and is also
CC expressed in some non-testicular cancers (of colon, pancreas, prostate
CC and ovary), so is a marker/potential therapeutic target for cancer. The
CC promoter from the HELA2 gene is useful for testis-specific expression of
CC other genes, e.g. for gene therapy or modulation of fertility. Drugs that
CC block activity of HELA2 should have antitumour activity (other than in
CC testis) while in testis recombinant HELA2 should stop growth of tumours
CC and normalise sperm development (eliminating the need for orchidectomy).
CC Identification of mutant forms of HELA2 can be used to diagnose
CC infertility
XX SQ Sequence 1100 BP; 226 A; 319 C; 313 G; 242 T; 0 U; 0 Other;

[illegible]

661	GGACATCTTTGGAGACATGGTTTGTCTGGCAATGCCAAGGGCGGAGGATGCCTGCTT	720
721	CGTGACTCAGGTGGACCCCTTGGCCCTGTAAACAAGGATGGACTGTGTATCAGATTGGAGT	780
721	CGTGACTCAGGTGGACCCCTTGGCCCTGTAAACAAGGATGGACTGTGTATCAGATTGGAGT	780
781	CGTGAGCTGGGAGTGGGCTGTGGTTCGGCCCAATCGGCCGGTGTCTACACCAATATCAG	840
781	CGTGAGCTGGGAGTGGGCTGTGGTTCGGCCCAATCGGCCGGTGTCTACACCAATATCAG	840
841	CCACCACTTTGAGTGGATCCAGAAAGCTGATGGCCAGAGTGGCATGTCCAGCCAGACCC	900
841	CCACCACTTTGAGTGGATCCAGAAAGCTGATGGCCAGAGTGGCATGTCCAGCCAGACCC	900
901	CTCCTGGCCGCTACTCTTTTTTCCCTCTTCTCTGGGCTCTCCCACTCCTGGGGCCGCTGTG	960
901	CTCCTGGCCGCTACTCTTTTTTCCCTCTTCTCTGGGCTCTCCCACTCCTGGGGCCGCTGTG	960
961	AGCCTACTTGAGCCCATGACGCTGGGGCCCATGCGCAAGTCAGGCCCTGTGTTCTCTTCTG	1020
961	AGCCTACTTGAGCCCATGACGCTGGGGCCCATGCGCAAGTCAGGCCCTGTGTTCTCTTCTG	1020
1021	TCTTGTGTTGGTAAATAACACATTCACATTCACATTCAGTTGATGCCTTGAGGGCAATTTTCAAAAAAAA	1080
1021	TCTTGTGTTGGTAAATAACACATTCACATTCACATTCAGTTGATGCCTTGAGGGCAATTTTCAAAAAAAA	1080
1081	AAAAAAAAAAAAAAAAAAAAA 1100	
1081	AAAAAAAAAAAAAAAAAAAAA 1100	
RESULT 2		
AA52259		
ID	AA52259 standard; DNA; 1100 BP.	
XX	AA52259;	
AC		
XX		
XX	25-JUN-1999 (first entry)	
XX		
DE	Protein PRO303 cDNA clone DNA42551-1217.	
XX		
KW	Secreted protein; transmembrane protein; human; enterocolitis;	
KW	Zollinger-Ellison syndrome; gastrointestinal ulceration;	
KW	congenital microvillus atrophy; skin disease; cell growth;	
KW	abnormal keratinocyte differentiation; psoriasis; epithelial cancer;	
KW	Parkinson's disease; Alzheimer's disease; ALS; neuropathy; fibromodulin;	
KW	dermal scarring; Usher Syndrome; Atrophia areata; anti-thrombotic;	
KW	wound healing; tissue repair; ss.	
OS	Homo sapiens.	
XX		
PN	WO9914328-A2.	
XX		
PD	25-MAR-1999.	
XX		
XX	16-SEP-1998; 98WO-US019330.	
PR	17-SEP-1997; 97US-0059113P.	
PR	17-SEP-1997; 97US-0059115P.	
PR	17-SEP-1997; 97US-0059117P.	
PR	17-SEP-1997; 97US-0059119P.	
PR	17-SEP-1997; 97US-0059121P.	
PR	17-SEP-1997; 97US-0059122P.	
PR	17-SEP-1997; 97US-0059184P.	
PR	18-SEP-1997; 97US-0059263P.	
PR	18-SEP-1997; 97US-0059266P.	
PR	15-OCT-1997; 97US-0062125P.	
PR	17-OCT-1997; 97US-0062285P.	
PR	17-OCT-1997; 97US-0062287P.	
PR	21-OCT-1997; 97US-0063486P.	
PR	24-OCT-1997; 97US-0062814P.	
PR	24-OCT-1997; 97US-0062816P.	
PR	24-OCT-1997; 97US-0063045P.	

PR	24-OCT-1997;	97US-0063120P.	
PR	24-OCT-1997;	97US-0063121P.	
PR	24-OCT-1997;	97US-0063127P.	
PR	24-OCT-1997;	97US-0063128P.	
PR	27-OCT-1997;	97US-0063327P.	
PR	27-OCT-1997;	97US-0063329P.	
PR	28-OCT-1997;	97US-0063541P.	
PR	28-OCT-1997;	97US-0063542P.	
PR	28-OCT-1997;	97US-0063544P.	
PR	28-OCT-1997;	97US-0063549P.	
PR	28-OCT-1997;	97US-0063550P.	
PR	28-OCT-1997;	97US-0063564P.	
PR	29-OCT-1997;	97US-0063435P.	
PR	29-OCT-1997;	97US-0063704P.	
PR	29-OCT-1997;	97US-0063732P.	
PR	29-OCT-1997;	97US-0063734P.	
PR	29-OCT-1997;	97US-0063735P.	
PR	29-OCT-1997;	97US-0063738P.	
PR	29-OCT-1997;	97US-0064215P.	
PR	31-OCT-1997;	97US-0063870P.	
PR	31-OCT-1997;	97US-0064103P.	
PR	03-NOV-1997;	97US-0064248P.	
PR	07-NOV-1997;	97US-0064809P.	
PR	12-NOV-1997;	97US-0065186P.	
PR	17-NOV-1997;	97US-0065846P.	
PR	18-NOV-1997;	97US-0065693P.	
PR	21-NOV-1997;	97US-0066120P.	
PR	21-NOV-1997;	97US-0066364P.	
PR	24-NOV-1997;	97US-0066453P.	
PR	24-NOV-1997;	97US-0066466P.	
PR	24-NOV-1997;	97US-0066511P.	
PR	24-NOV-1997;	97US-0066770P.	
PR	24-NOV-1997;	97US-0066772P.	
PR	25-NOV-1997;	97US-0066840P.	
XX			
XX	(GETH) GENENTECH INC.		
XX			
XX	Wood WI, Gurney AL, Goddard A, Pennica D, Chen J, Yuan J;		
PI	WPI; 1999-229533/19.		
DR	P-PSDB; AAV13388.		
DR			
XX			
PT	New isolated human genes and polypeptides used in, e.g. treatment of		
PT	Gastrointestinal ulceration.		
PS	Claim 2; Fig 91; 320pp; English.		
XX			
XX	AAX5213-74 encode secreted and transmembrane human proteins, and are		
CC	obtained from cDNA libraries, prepared from fetal lung, fetal kidney,		
CC	fetal brain, fetal liver and fetal retina. The encoded polypeptides have		
CC	specific uses based on their homology to known polypeptides, e.g. PRO211		
CC	and PRO217 can be used for disorders associated with the preservation and		
CC	maintenance of gastrointestinal mucosa and the repair of acute and		
CC	chronic mucosal lesions (e.g. enterocolitis, Zollinger-Ellison syndrome,		
CC	gastrointestinal ulceration and congenital microvillus atrophy), skin		
CC	diseases associated with abnormal keratinocyte differentiation (e.g.		
CC	psoriasis, epithelial cancers such as lung squamous cell carcinoma of the		
CC	vulva and gliomas), potent effects on cell growth and development,		
CC	diseases related to growth or survival of nerve cells including		
CC	Parkinson's disease, Alzheimer's disease, ALS, neuropathies or cancer.		
CC	PRO265 can be used as for fibromodulin, e.g. for reducing dermal		
CC	scarring. PRO264 can be used as a target for anti-tumor drugs. PRO533 may		
CC	be used in the treatment of Usher Syndrome or Atrophia areata; PRO269 can		
CC	be used as an anti-thrombotic agent; PRO287 polypeptides and portions may		
CC	have therapeutic applications in wound healing and tissue repair; PRO317		
CC	can be used for treating problems of the kidney, uterus, endometrium,		
CC	blood vessels, or related tissue, e.g. in the heart of genital tract		
XX			
SQ	Sequence 1100 BP; 225 A; 321 C; 314 G; 240 T; 0 U; 0 Other;		
Query Match	99.1%; Score 1090.6; DB 2; Length 1100;		
Best Local Similarity	99.6%; Fred. No. 4.4e-227;		
Matches 1093; Conservative	0; Mismatches 4; Indels		
	0; Gaps		

```
Query Match      99.1%; Score 1090.6; DB 2; Length 1100;
Best Local Similarity 99.6%; Pred. No. 4.4e-227;
Matches 1093; Conservative 0; Mismatches 4; Indels 0; Gaps 0
```

Qy	1	CGCGGAGAGGACGCCATGCGCGCGCGCGCGCGCTGCTCTGCGCGCTGCTGCTGCGCTG	60
Db	4	CGCGGAGAGGAGGCGCATGCGCGCGCGCGCGCGCGCTGCTGCTGCGCGCTGCTGCTGCGCTG	63
Qy	61	GGCTGGACTCAGGAAGCCGAGTTCGACGAGGCGGCGCGCTTATCAGGACCATCGCGCGCG	120
Db	64	GGCTGGACTCAGGAAGCCGAGTTCGACGAGGCGGCGCGCTTATCAGGACCATCGCGCGCG	123
Qy	121	ACGGGTCACTACGTCGGGCATTCGTGGGTGAGAGGACGCCGAACCTCGGGCGTTGGCGCGTG	180
Db	124	ACGGGTCACTACGTCGGGCATTCGTGGGTGAGAGGACGCCGAACCTCGGGCGTTGGCGCGTG	183
Qy	181	GCAGGGAGGCGCTCGCGCTGTGGGATTTCCACGTTATGCGAGTGCAGCTGCTCAGCCACCG	240
Db	184	GCAGGGAGGCGCTCGCGCTGTGGGATTTCCACGTTATGCGAGTGCAGCTGCTCAGCCACCG	243
Qy	241	CTGGGCACCTACGCGCGCGCACCTGCTTTGAAACCTATAGTGACCTTAGTGATCCCTCCGG	300
Db	244	CTGGGCACCTACGCGCGCGCACCTGCTTTGAAACCTATAGTGACCTTAGTGATCCCTCCGG	303
Qy	301	GTGGATGTCGAGTTTGGCCAGCTGATCCATGCCATCCTTCTGAGCCTGCAGGCTTA	360
Db	304	GTGGATGTCGAGTTTGGCCAGCTGATCCATGCCATCCTTCTGAGCCTGCAGGCTTA	363
Qy	361	CTACACCCGTTACTTCGTATCGAATATCTATCTGAGCCCTCGTACTCTGGGAATTCACC	420
Db	364	CTACACCCGTTACTTCGTATCGAATATCTATCTGAGCCCTCGTACTCTGGGAATTCACC	423
Qy	421	CTATGACATTTGCTTGGTGAGCTGTCTGCACCTGTCACTACATAACACATCCAGCC	480
Db	424	CTATGACATTTGCTTGGTGAGCTGTCTGCACCTGTCACTACATAACACATCCAGCC	483
Qy	481	CATCTGTCTCCAGGCTCCACATTTGAGTTTGAGAACCGGACAGACTGCTGGGTGACTGG	540
Db	484	CATCTGTCTCCAGGCTCCACATTTGAGTTTGAGAACCGGACAGACTGCTGGGTGACTGG	543
Qy	541	CTGGGGGTACATCAAGAGGATGAGGACCTGCCATCTCCCCACACCCCTCCAGGAAGTTCA	600
Db	544	CTGGGGGTACATCAAGAGGATGAGGACCTGCCATCTCCCCACACCCCTCCAGGAAGTTCA	603
Qy	601	GGTGGCCATCATAAACAACTCTATGTGCAACCACTTCTCTCAAGTACAGTTTCCGCAA	660
Db	604	GGTGGCCATCATAAACAACTCTATGTGCAACCACTTCTCTCAAGTACAGTTTCCGCAA	663
Qy	661	GGACATCTTTGGAGACATGGTTTGTCTGGCAATGCCAAGCGCGGAAGATGCCCTGCTT	720
Db	664	GGACATCTTTGGAGACATGGTTTGTCTGGCAATGCCAAGCGCGGAAGATGCCCTGCTT	723
Qy	721	CGGTGACTCAGTGGGACCTTTGGCCCTGTAAACAGGATGGAATCTGTGTATCAGATTTGAGT	780
Db	724	CGGTGACTCAGTGGGACCTTTGGCCCTGTAAACAGGATGGAATCTGTGTATCAGATTTGAGT	783
Qy	781	CGTGAGCTGGGAGTGGGCTGTGGTGGCCCAATCGGCCCGGTCTCACACCAATATCAG	840
Db	784	CGTGAGCTGGGAGTGGGCTGTGGTGGCCCAATCGGCCCGGTCTCACACCAATATCAG	843
Qy	841	CCACCACTTTGAGTGGATCCAGAAGCTGATGGCCACAGAGTGGCATCTCCAGCCAGACCC	900
Db	844	CCACCACTTTGAGTGGATCCAGAAGCTGATGGCCACAGAGTGGCATCTCCAGCCAGACCC	903
Qy	901	CTCCTGGCGCTACTCTTTTTCCTTCTCTGGGCTCTCCCACTCTCTGGGCGCGGTCTG	960
Db	904	CTCCTGGCGCTACTCTTTTTCCTTCTCTGGGCTCTCCCACTCTCTGGGCGCGGTCTG	963
Qy	961	AGCCTACCTGAGCCCATGACGCTGGGGCCACTGCCCCAAGTCAGGCCCTGGTCTCTTCTG	1020
Db	964	AGCCTACCTGAGCCCATGACGCTGGGGCCACTGCCCCAAGTCAGGCCCTGGTCTCTTCTG	1023
Qy	1021	TCTGTGTTGGTAAATAACAATTCAGTTGATGCCCTTGACGGGCAATTTTCAAAAAAAA	1080
Db	1024	TCTGTGTTGGTAAATAACAATTCAGTTGATGCCCTTGACGGGCAATTTTCAAAAAAAA	1083

QY 1081 AAAAAAAAAAAAAA 1097
DB 1084 AAAAAAAAAAAAAA 1100

RESULT 3
ID ADC78568 standard; cDNA; 1100 BP.
XX AC ADC78568;
XX 01-JAN-2004 (first entry)
XX DE Human PRO303 cDNA.

KW antiinflammatory; antiulcer; cytostatic; antipsoriatic; antiparkinsonian;
KW neurotrophic; neuroprotective; vasotropic; chemotactic; angiogenic;
KW neurotrophic; osteopathic; antiasthmatic; antiarthritic; antirheumatic;
KW antiarteriosclerotic; cardiant; antidiabetic; cerebroprotective;
KW thrombolytic; immunomodulator; enterocolitis; Zollinger-Ellison syndrome;
KW gastrointestinal ulceration; psoriasis; cancer; Parkinson's disease;
KW Alzheimer's; ALS; neuropathy; dermal scarring; wound healing;
KW nerve repair; thrombosis; bone; cartilage formation; angiogenesis;
KW asthma; rheumatoid arthritis; multiple sclerosis; inflammatory disorder;
KW atherosclerosis; cardiac injury; infertility; premature aging; AIDS;
KW diabetes; stroke; gene therapy; transgenic; PRO; human; ss; gene.
XX OS Homo sapiens.

XX WO2000015796-A2.
XX PD 23-MAR-2000.
XX PF 15-SEP-1999; 99WO-US021090.
XX PR 16-SEP-1998; 99WO-US019330.
XX PA (GETH) GENENTECH INC.
PI Chen J, Goddard A, Gurney AL, Hillan K, Pennica D, Wood WJ;
PI Yuan J;
XX WPI; 2000-271434/23.
DR P-PSDB; ADC78569.

XX Novel nucleic acids encoding secreted and transmembrane polypeptides with
PT homology, e.g. to growth and cancer-associated antigens.
XX Claim 2; SEQ ID NO 256; 355pp; English.

XX The invention relates to a novel nucleic acid encoding a PRO polypeptide.
XX The polypeptides and polynucleotides of the invention may be useful as
XX research tools and as therapeutics for treating enterocolitis, Zollinger-
XX Ellison syndrome, gastrointestinal ulceration, psoriasis, cancer,
XX Parkinson's disease, Alzheimer's disease, ALS, neuropathies, dermal
XX scarring and wound healing, nerve repair, thrombosis, bone and/or
XX cartilage formation, angiogenesis, asthma, rheumatoid arthritis, multiple
XX sclerosis, inflammatory disorders, atherosclerosis, cardiac injury,
XX infertility, premature aging, AIDS, diabetes complications and stroke.
XX The molecules may also be utilised during gene therapy procedures and
XX transgenic animal production. The current sequence is that of the human
XX PRO cDNA of the invention.

XX Sequence 1100 BP; 225 A; 321 C; 314 G; 240 T; 0 U; 0 Other;

Query Match 99.1%; Score 1090.6; DB 3; Length 1100;
Best Local Similarity 99.6%; Pred. No. 4.4e-227;
Matches 1093; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGCGGAGAGGAGCCATGGCGCGCGCGCGCGCTGCTGCTGGCGCTGCTGCTGGCTCG 60
DB 4 CGCGGAGAGGAGCCATGGCGCGCGCGCGCGCTGCTGCTGGCGCTGCTGCTGGCTCG 63

QY 61 GGCTGGACTCAGGAAGCCGGAGTCGAGGAGCGCGCCGCTTATCAGGACCATCGCGCG 120
DB 64 GGCTGGACTCAGGAAGCCGGAGTCGAGGAGCGCGCCGCTTATCAGGACCATCGCGCG 123

QY 121 ACGGTCATCAGCTCGCGCATCGTGGTGGAGAGAGCCGAACTCGGGCGTTGGCGCTG 180
DB 124 ACGGTCATCAGCTCGCGCATCGTGGTGGAGAGAGAGCGCGAACTCGGGCGTTGGCGCTG 183

QY 181 GCAGGGAGAGCTCGCGCTGTTGGATTCGCCACGTATGCGAGTGGAGCTGCTCAGGACAC 240
DB 184 GCAGGGAGAGCTCGCGCTGTTGGATTCGCCACGTATGCGAGTGGAGCTGCTCAGGACAC 243

QY 241 CTGGGCACTCACGGCGCGCACTGCTTTGAAACCTATAGTGACCTTAGTGATCCCTCCGG 300
DB 244 CTGGGCACTCACGGCGCGCACTGCTTTGAAACCTATAGTGACCTTAGTGATCCCTCCGG 303

QY 301 GTGATGGTTCAGTTGGCCAGCTGATTCATGCCATCCCTCTCGAGCCTCGAGGCTA 360
DB 304 GTGATGGTTCAGTTGGCCAGCTGATTCATGCCATCCCTCTCGAGCCTCGAGGCTA 363

QY 361 CTACACCCGTTACTTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGGAATTCACC 420
DB 364 CTACACCCGTTACTTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGGAATTCACC 423

QY 421 CTATGACATTCGCTTGGTGAAGCTGTCTGCACCTGTACCTACACTACATAACACATCCAGCC 480
DB 424 CTATGACATTCGCTTGGTGAAGCTGTCTGCACCTGTACCTACACTACATAACACATCCAGCC 483

QY 481 CATCTGCTCCAGGCTCCACATTTGAGTTGAGAACCGGACAGACTGCTGGGTGACTGG 540
DB 484 CATCTGCTCCAGGCTCCACATTTGAGTTGAGAACCGGACAGACTGCTGGGTGACTGG 543

QY 541 CTGGGGTACATCAAGAGGATGAGGCACTGTCATCTCCCAACACCTCTCAGGAAGTTCA 600
DB 544 CTGGGGTACATCAAGAGGATGAGGCACTGTCATCTCCCAACACCTCTCAGGAAGTTCA 603

QY 601 GGTGCGCATCATAAACAACTCTATGTGCAACACCTCTTCTCAAGTACAGTTTCGCGAA 660
DB 604 GGTGCGCATCATAAACAACTCTATGTGCAACACCTCTTCTCAAGTACAGTTTCGCGAA 663

QY 661 GGACATCTTTGGAGACATGGTTTGTGCTGGCAATGCCAAGCGGGAAGATGCTGCTT 720
DB 664 GGACATCTTTGGAGACATGGTTTGTGCTGGCAATGCCAAGCGGGAAGATGCTGCTT 723

QY 721 CGGTGACTCAGGTGGACCTTGGCTGTAAAGGATGGAATGCTGTGATCAGATTGGAGT 780
DB 724 CGGTGACTCAGGTGGACCTTGGCTGTAAAGGATGGAATGCTGTGATCAGATTGGAGT 783

QY 781 CGTGAGCTGGGAGTGGGTGGTGGGCCAATCGGCCGCTGTCTACACCAATATCAG 840
DB 784 CGTGAGCTGGGAGTGGGTGGTGGGCCAATCGGCCGCTGTCTACACCAATATCAG 843

QY 841 CCACCATTTGAGTGGATCCAGAGCTGATGGCCAGAGTGGCATGTCCAGCGCAGNCCC 900
DB 844 CCACCATTTGAGTGGATCCAGAGCTGATGGCCAGAGTGGCATGTCCAGCGCAGNCCC 903

QY 901 CTCTGGCCCTACTCTTTTCTCTCTGGGCTCTCCCACTCTCTGGGCGGGTCTG 960
DB 904 CTCTGGCCCTACTCTTTTCTCTCTGGGCTCTCCCACTCTCTGGGCGGGTCTG 963

QY 961 AGCCTACCTGAGCCCATGAGCTGGGGCAGCTGCCAAGTCAGGCCCTGGTCTCTTCTG 1020
DB 964 AGCCTACCTGAGCCCATGAGCTGGGGCAGCTGCCAAGTCAGGCCCTGGTCTCTTCTG 1023

QY 1021 TCTTTGTTGGTAATAACACATTCGAGTTGATGCTTGGAGGCAATTTTCAAAAAA 1080
DB 1024 TCTTTGTTGGTAATAACACATTCGAGTTGATGCTTGGAGGCAATTTTCAAAAAA 1083

QY 1081 AAAAAAAAAAAAAA 1097
DB 1084 AAAAAAAAAAAAAA 1100

transgenic animals or knock-out animals which may be used in the development and screening of therapeutically useful reagents. The nucleic acids may also be used in gene therapy, in chromosome identification, as chromosome markers, or in generating probes. The PRO polypeptides are useful as molecular markers for protein electrophoresis, and the isolated nucleic acids may be used for recombinantly expressing those markers. The PRO polypeptides and nucleic acids may also be used in tissue typing. Anti-PRO antibodies are useful in diagnostic assays for PRO, and in affinity purification of PRO from recombinant cell culture or natural sources. The present sequence encodes a PRO protein

SQ Sequence 1100 BP; 225 A; 321 C; 314 G; 240 T; 0 U; 0 Other;

Query Match 99.1%; Score 1090.6; DB 8; Length 1100;
Best Local Similarity 99.6%; Pred. No. 4.4e-227;
Matches 1093; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy 1 CGCGGAGAGGAGCCATGGCGCGCGCGCGCGCGCTGCTGCGCGCTGCTGGCGCTGCTGGCTCG 60
Db 4 CGCGGAGAGAGGCCATGGCGCGCGCGCGCGCGCTGCTGCTGGCGCTGCTGGCTCG 63

Qy 61 GGTGAGCTCAGGAGCGGAGTGCAGAGAGCGCGCGCGCTTATCAGGACCATCGCGCG 120
Db 64 GGTGAGCTCAGGAGCGGAGTGCAGAGAGCGCGCGCGCTTATCAGGACCATCGCGCG 123

Qy 121 ACGGGTATCAGTGCAGCGCATGCTGGGTGGAGAGAGCGCGGAACTCGGGCGTTGGCGGTG 180
Db 124 ACGGGTATCAGTGCAGCGCATGCTGGGTGGAGAGAGCGCGGAACTCGGGCGTTGGCGGTG 183

Qy 181 GCAGGGAGCGTGGCGCTGCGGATTCACGATGCGGAGTGCAGCGCTGCTCAGCCACCG 240
Db 184 GCAGGGAGCGTGGCGCTGCGGATTCACGATGCGGAGTGCAGCGCTGCTCAGCCACCG 243

Qy 241 CTGGGCACTCAGCGCGCGCACTGCTTTGAAACCTATAGTGACCTTAGTGATCCCTCCGG 300
Db 244 CTGGGCACTCAGCGCGCGCACTGCTTTGAAACCTATAGTGACCTTAGTGATCCCTCCGG 303

Qy 301 GTGANTGTCAGTTTGGCCAGCTGACTTCCATGTCATCTTCTGGAGCCTGCGAGGCTA 360
Db 304 GTGANTGTCAGTTTGGCCAGCTGACTTCCATGTCATCTTCTGGAGCCTGCGAGGCTA 363

Qy 361 CTACACCGTTACTTCGTATCGATATCTATCTGAGCCCTCGCTACCTGGGGAAATTCAC 420
Db 364 CTACACCGTTACTTCGTATCGATATCTATCTGAGCCCTCGCTACCTGGGGAAATTCAC 423

Qy 421 CTATGACATTCCTTGTGTGAAGCTGTCTGCACCTGTCTACCTACACTAAACATCCAGCC 480
Db 424 CTATGACATTCCTTGTGTGAAGCTGTCTGCACCTGTCTACCTACACTAAACATCCAGCC 483

Qy 481 CATCTGTCTCAGGCTCCACATTTGAGTTTGAACCCGGAACAGACTGCTGGGTGACTGG 540
Db 484 CATCTGTCTCAGGCTCCACATTTGAGTTTGAACCCGGAACAGACTGCTGGGTGACTGG 543

Qy 541 CTGGGGTACATCAAGAGGATAGGCACTGCCATCTCCCAACCTCCAGGAGTTCA 600
Db 544 CTGGGGTACATCAAGAGGATAGGCACTGCCATCTCCCAACCTCCAGGAGTTCA 603

Qy 601 GGTGCCATCATAAACAACTCTATGTGCAACACACCTCTTCTCAAGTACAGTTTCGCGAA 660
Db 604 GGTGCCATCATAAACAACTCTATGTGCAACACACCTCTTCTCAAGTACAGTTTCGCGAA 663

Qy 661 GGAATCTTTTGAGACATGTTTGTGTGGCAATGCCCAAGCGGGAGAGATGCTGCTT 720
Db 664 GGAATCTTTTGAGACATGTTTGTGTGGCAATGCCCAAGCGGGAGAGATGCTGCTT 723

Qy 721 CGGTGACTCAGTGGACCTTGGCTGTAAACAGAGTGAAGTGTGATCAGATGGAGT 780
Db 724 CGGTGACTCAGTGGACCTTGGCTGTAAACAGAGTGAAGTGTGATCAGATGGAGT 783

Qy 781 CGTGAAGTGGGAGTGGGCTGTGGTGGCGCCCAATCGGGCCCGGTGTCTACACCAATATCAG 840
Db 784 CGTGAAGTGGGAGTGGGCTGTGGTGGCGCCCAATCGGGCCCGGTGTCTACACCAATATCAG 843
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Qy 841 CCACCACTTTCAGTGGATCCAGAGCTGATGCGCCAGAGTGGCATGTCCAGCCAGACCC 900
Db 844 CCACCACTTTCAGTGGATCCAGAGCTGATGCGCCAGAGTGGCATGTCCAGCCAGACCC 903

Qy 901 CTCCTGGCCGCTACTCTTTTCCCTCTTCTCTGGGCTCTCCCACTCTCTGGGCGCGGTCTG 960
Db 904 CTCCTGGCCGCTACTCTTTTCCCTCTTCTCTGGGCTCTCCCACTCTCTGGGCGCGGTCTG 963

Qy 961 AGCTACTGAGCCCATCGACGCTTGGGGCCACTGCCAAGTCAGGCCCTCTTCTTCTCTG 1020
Db 964 AGCTACTGAGCCCATCGACGCTTGGGGCCACTGCCAAGTCAGGCCCTCTTCTTCTCTG 1023

Qy 1021 TCTTGTGTTGTTAATAAACACATTCAGTTCAGTTCAGTTCAGGCGCATTTTCAAAAAAAA 1080
Db 1024 TCTTGTGTTGTTAATAAACACATTCAGTTCAGTTCAGTTCAGGCGCATTTTCAAAAAAAA 1083

Qy 1081 AAAAAAATAAAAAA 1097
Db 1084 AAAAAAATAAAAAA 1100

RESULT 6
ACD07611
ID ACD07611 standard; cDNA; 1100 BP.
XX ACD07611;
AC ACD07611;
XX
DT 07-AUG-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO303 cDNA.
XX
KW Human; secreted and transmembrane protein; PRO; pharmaceutical;
diagnostic; biosensor; bioeffector; Parkinson's disease;
KW Alzheimer's disease; inflammation; nephritis; wound healing;
KW nerve repair; collateral blood vessel formation; cancer;
KW colorectal cancer; haemorrhage; rheumatoid arthritis; diabetes;
KW cirrhosis; fibrosis; restenosis; dermal fibrotic condition; keloid;
KW scarring; ischaemia; stroke; hypertension; heart attack; atherosclerosis;
KW infertility; gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
PN US2002197671-A1.
XX
PD 26-DEC-2002.
XX
PF 17-JUL-2001; 2001US-00507824.
XX
PR 17-SEP-1997; 97US-0059113P.
PR 17-SEP-1997; 97US-0059115P.
PR 17-SEP-1997; 97US-0059117P.
PR 17-SEP-1997; 97US-0059119P.
PR 17-SEP-1997; 97US-0059121P.
PR 17-SEP-1997; 97US-0059122P.
PR 17-SEP-1997; 97US-0059184P.
PR 18-SEP-1997; 97US-0059266P.
PR 18-SEP-1997; 97US-0062125P.
PR 15-OCT-1997; 97US-0062125P.
PR 17-OCT-1997; 97US-0062285P.
PR 17-OCT-1997; 97US-0062287P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0062814P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063045P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 24-OCT-1997; 97US-0063127P.
PR 24-OCT-1997; 97US-0063128P.
PR 27-OCT-1997; 97US-0063327P.
PR 27-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063542P.
PR 28-OCT-1997; 97US-0063544P.
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PR	28-OCT-1997;	97US-0063549P.
PR	28-OCT-1997;	97US-0063550P.
PR	28-OCT-1997;	97US-0063564P.
PR	29-OCT-1997;	97US-0063435P.
PR	29-OCT-1997;	97US-0063704P.
PR	29-OCT-1997;	97US-0063732P.
PR	29-OCT-1997;	97US-0063734P.
PR	29-OCT-1997;	97US-0063735P.
PR	29-OCT-1997;	97US-0063738P.
PR	29-OCT-1997;	97US-0064215P.
PR	31-OCT-1997;	97US-0063870P.
PR	31-OCT-1997;	97US-0064103P.
PR	03-NOV-1997;	97US-0064248P.
PR	07-NOV-1997;	97US-0064809P.
PR	12-NOV-1997;	97US-0065186P.
PR	17-NOV-1997;	97US-0065846P.
PR	18-NOV-1997;	97US-0065693P.
PR	21-NOV-1997;	97US-0066120P.
PR	21-NOV-1997;	97US-0066364P.
PR	24-NOV-1997;	97US-0066453P.
PR	24-NOV-1997;	97US-0066466P.
PR	24-NOV-1997;	97US-0066511P.
PR	24-NOV-1997;	97US-0066770P.
PR	24-NOV-1997;	97US-0066772P.
PR	10-SEP-1998;	98WO-US018824.
PR	14-SEP-1998;	98WO-US019177.
PR	16-SEP-1998;	98WO-US019330.
PR	17-SEP-1998;	98WO-US019437.
PR	01-DEC-1998;	98WO-US025108.
PR	08-SEP-1999;	99WO-US020594.
PR	13-SEP-1999;	99WO-US020944.
PR	15-SEP-1999;	99WO-US021090.
PR	15-SEP-1999;	99WO-US021547.
PR	05-OCT-1999;	99WO-US023089.
PR	29-NOV-1999;	99WO-US028214.
PR	30-NOV-1999;	99WO-US028313.
PR	01-DEC-1999;	99WO-US028301.
PR	02-DEC-1999;	99WO-US028564.
PR	02-DEC-1999;	99WO-US028565.
PR	16-DEC-1999;	99WO-US030095.
PR	20-DEC-1999;	99WO-US030911.
PR	20-DEC-1999;	99WO-US030999.
PR	05-JAN-2000;	2000WO-US000219.
PR	11-FEB-2000;	2000WO-US003565.
PR	24-FEB-2000;	2000WO-US004414.
PR	24-FEB-2000;	2000WO-US005004.
PR	02-MAR-2000;	2000WO-US005841.
PR	30-MAR-2000;	2000WO-US007377.
PR	30-MAR-2000;	2000WO-US008439.
PR	22-MAY-2000;	2000WO-US014042.
PR	02-JUN-2000;	2000WO-US015264.
PR	28-JUL-2000;	2000WO-US020710.
PR	24-AUG-2000;	2000WO-US023328.
PR	18-SEP-2000;	2000US-00665350.
XX		
PA	(GETH) GENENTECH INC.	
XX		
PI	Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;	
PI	Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;	
PI	Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kijavlin IJ;	
PI	Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;	
PI	Williams PM, Wood WI;	
DR	WFI; 2003-370793/35.	
DR	P-PSDB; ABO01818.	
XX		
PT	New genes and secreted and transmembrane polypeptides (e.g. PRO245 or	
PT	PRO335), useful for treating or diagnosing e.g. Alzheimer's disease,	
PT	cancers, hemorrhage, rheumatoid arthritis, diabetes, cirrhosis, ischemia	
PT	or strokes.	
XX		
XX	Claim 2; Fig 91; 482pp; English.	
XX		

CC	The invention describes a new isolated nucleic acid molecule comprising
CC	the full length coding sequence of the DNA deposited with the American
CC	Type Culture Collection (e.g. ATCC Deposit No. 209258) or a sequence
CC	with at least 80% identity to a DNA encoding a PRO polypeptide comprising
CC	any of 61 sequences having 164-1119 amino acids fully defined in the
CC	specification. The PRO polypeptides or polynucleotides are useful as
CC	pharmaceuticals, diagnostics, biosensors or bioreactors. These are
CC	particularly useful for detecting or treating e.g. Parkinson's disease,
CC	Alzheimer's disease, inflammations, nephritis, wound healing, nerve
CC	repair, collateral blood vessel formation, cancers (e.g. colorectal
CC	cancer), haemorrhage (or reduce risk for haemorrhage), rheumatoid
CC	arthritis, diabetes, cirrhosis of the liver, fibrosis of the lungs,
CC	restenosis, dermal fibrotic conditions (e.g. keloids or scarring), or
CC	ischaemia, strokes, hypertension, heart attacks, atherosclerosis, or
CC	infertility in mammals (e.g. humans, dogs, cats, cattle, horses, sheep,
CC	pigs, goats, or rabbits) The PRO polypeptides are useful as targets for
CC	therapeutic intervention in these diseases, and diagnostic determination
CC	of the presence of these diseases. The PRO polypeptides are also useful
CC	as molecular weight markers, or for chromosome identification. The PRO
CC	genes are useful as hybridisation probes, or for screening libraries of
CC	human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene
CC	therapy, particularly for replacing a defective gene. This sequence
CC	encodes a novel human secreted and transmembrane PRO polypeptide
XX	
SQ	Sequence 1100 BP; 225 A; 321 C; 314 G; 240 T; 0 U; 0 Other;
	Query Match 99.1%; Score 1090.6; DB 8; Length 1100;
	Best Local Similarity 99.6%; Pred. No. 4.4e-227;
	Matches 1093; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY	1 CGCGGGAGAGAGGCCATGGCGCGCGCGGGCGCTGCTGTGGCGCTGTCTGGGCTCG 60
DB	4 CGCGGGAGAGAGGCCATGGCGCGCGCGGGCGCTGCTGTGGCGCTGTCTGGGCTCG 63
QY	61 GGCTGGACTCAGGAAGCCGAGTGCAGGAGGGCGGCCGCTTATCAGAACCATCGGCGC 120
DB	64 GGCTGGACTCAGGAAGCCGAGTGCAGGAGGGCGGCCGCTTATCAGAACCATCGGCGC 123
QY	121 ACGGGTCATACGTCGGCGATCGTGGGTGAGGAGAGCGCGAACTCGGGCGTTGGCCGTG 180
DB	124 ACGGGTCATACGTCGGCGCATCGTGGGTGAGGAGAGCGCGAACTCGGGCGTTGGCCGTG 183
QY	181 GCAGGGGAGCGCTGCGCCTGTGGGATTCGCCAGTATGGCGAGTGAAGCTGTCTCAGCCACCG 240
DB	184 GCAGGGGAGCGCTGCGCCTGTGGGATTCGCCAGTATGGCGAGTGAAGCTGTCTCAGCCACCG 243
QY	241 CTGGGCACTCAGCGCGCGCACTGCTTTGAAACCTATAGTGACCTTAGTGATCCCTCCGG 300
DB	244 CTGGGCACTCAGCGCGCGCACTGCTTTGAAACCTATAGTGACCTTAGTGATCCCTCCGG 303
QY	301 GTGGATGGTCAGTTTGGCCAGCTGACTTCGATGCCATCCTTCTGGAGACCTGCAGGGCCTA 360
DB	304 GTGGATGGTCAGTTTGGCCAGCTGACTTCGATGCCATCCTTCTGGAGACCTGCAGGGCCTA 363
QY	361 CTACACCCGTTACTTCGTATCGAATATCTATCTGAGCGCCTCGCTPACCTGGGGAAATTCACC 420
DB	364 CTACACCCGTTACTTCGTATCGAATATCTATCTGAGCCCTCGCTPACCTGGGGAAATTCACC 423
QY	421 CTATGACATTTGCCCTTGGTGAAGCTGCTGCAACCTGTCAACCTACACTAAACACATCCAGCC 480
DB	424 CTATGACATTTGCCCTTGGTGAAGCTGCTGCAACCTGTCAACCTACACTAAACACATCCAGCC 483
QY	481 CATCTGTCACAGGCTTCACATTTGAGTTTGAGAACCGGACAGACTGCTGGGTGACTGG 540
DB	484 CATCTGTCACAGGCTTCACATTTGAGTTTGAGAACCGGACAGACTGCTGGGTGACTGG 543
QY	541 CTGGGGGTACATCAAGAGGATGAGGCACATGCCATCTCCCCACACCCCTCCAGGAAGTTTCA 600
DB	544 CTGGGGGTACATCAAGAGGATGAGGCACATGCCATCTCCCCACACCCCTCCAGGAAGTTTCA 603
QY	601 GGTGCGGCATATAAACAACTCTATGTGCAACCAACCTCTTCCCTCAAGTACAGTTTCCGCAA 660
DB	604 GGTGCGGCATATAAACAACTCTATGTGCAACCAACCTCTTCCCTCAAGTACAGTTTCCGCAA 663

CC purification of PRO from recombinant cell culture or natural sources. The
CC present sequence represents cDNA encoding a human secreted/transmembrane
CC PRO polypeptide

SQ Sequence 1100 BP; 225 A; 321 C; 314 G; 240 T; 0 U; 0 Other;
Query Match 99.1%; Score 1090.6; DB 8; Length 1100;
Best Local Similarity 99.6%; Pred. No. 4.4e-227;
Matches 1093; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy	1	CGCGGAGAGAGGCCATGCGGCGCGCGCGGCGCGTGTCTGTGGCGCTGTCTGTGGCTGTCTGTGGCTCG	60
Db	4	CGCGGAGAGAGGCCATGCGGCGCGCGCGGCGCGTGTCTGTGGCGCTGTCTGTGGCTGTCTGTGGCTCG	63
Qy	61	GGCTGGACTCAGGAAGCCGAGTGCAGAGGCGCGCGGTTATCAGAACCATGCGGCG	120
Db	64	GGCTGGACTCAGGAAGCCGAGTGCAGAGGCGCGCGGTTATCAGAACCATGCGGCG	123
Qy	121	ACGGGTCAATCAGCTCGCGCATCTGTGGGTGAGAGACGCCCAACTCGGCGGTGGCCCGT	180
Db	124	ACGGGTCAATCAGCTCGCGCATCTGTGGGTGAGAGAGCAGCCGAACTCGGCGGTGGCCCGT	183
Qy	181	GCAGGGAGCCTGCGCCTGTGGATTCCTCATGTGCGGAGTGAGCCTGTCTCAGCACCG	240
Db	184	GCAGGGAGCCTGCGCCTGTGGATTCCTCATGTGCGGAGTGAGCCTGTCTCAGCACCG	243
Qy	241	CTGGGCACTCACGGGGCGCACTGCTTTGAACCTATATAGTAGCCTTAGTAGTCCTCTCGG	300
Db	244	CTGGGCACTCACGGGGCGCACTGCTTTGAACCTATATAGTAGCCTTAGTAGTCCTCTCGG	303
Qy	301	GTGGATGTCTCAGTCTTGCCCACTGACTTCCATGCCATCTCTTCTGGAGCCTTGAGGCCCTA	360
Db	304	GTGGATGTCTCAGTCTTGCCCACTGACTTCCATGCCATCTCTTCTGGAGCCTTGAGGCCCTA	363
Qy	361	CTACACCGCTTACTCGTATCGAATATCTATCTGAGCCTCGTACCTGGGAAATTCACC	420
Db	364	CTACACCGCTTACTCGTATCGAATATCTATCTGAGCCTCGTACCTGGGAAATTCACC	423
Qy	421	CTATGACATTCGCTTGGTGAAGCTGTCTGCACCTGTCACTTACCTAAACACATCCAGCC	480
Db	424	CTATGACATTCGCTTGGTGAAGCTGTCTGCACCTGTCACTTACCTAAACACATCCAGCC	483
Qy	481	CATCTGTCTCAGCGCTCCACATTTAGTTTGAGAACCGGACAGACTCTCGGTGACTGG	540
Db	484	CATCTGTCTCAGCGCTCCACATTTAGTTTGAGAACCGGACAGACTCTCGGTGACTGG	543
Qy	541	CTGGGGGTACATCAAGAGGATGAGCACTGCCATCTCTCCCACTCTCCAGGAAGTTCA	600
Db	544	CTGGGGGTACATCAAGAGGATGAGCACTGCCATCTCTCCCACTCTCCAGGAAGTTCA	603
Qy	601	GGTCGCATCATAAACCACTTATGTCAACCACTCTTCTCAAGTACAGTTTCCGAA	660
Db	604	GGTCGCATCATAAACCACTTATGTCAACCACTCTTCTCAAGTACAGTTTCCGAA	663
Qy	661	GGACATCTTTGGAGACATGGTTTGTGTGGCAATGCCCAAGCGCGGAAGGATGCTGT	720
Db	664	GGACATCTTTGGAGACATGGTTTGTGTGGCAAGCCCAAGCGCGGAAGGATGCTGT	723
Qy	721	CGGTGATCTCAGGTGGACCTTTGGCCTGTAAACAAGATGGACTGTGGTATCAGATTGGAGT	780
Db	724	CGGTGATCTCAGGTGGACCTTTGGCCTGTAAACAAGATGGACTGTGGTATCAGATTGGAGT	783
Qy	781	CGTGAGCTGGGAGTGGCTGTGGTCGGCCCAATCGGCCCGGTGTCTACACCAATATCAG	840
Db	784	CGTGAGCTGGGAGTGGCTGTGGTCGGCCCAATCGGCCCGGTGTCTACACCAATATCAG	843
Qy	841	CCACCACTTTGAGTGGATCCAGAAAGCTGATGGCCACAGTGGCATGTCCACCGACAGACC	900
Db	844	CCACCACTTTGAGTGGATCCAGAAAGCTGATGGCCACAGTGGCATGTCCACCGACAGACC	903
Qy	901	CTCTCGCGCGCTACTCTTTTTTCCCTCTTCTCTGGGCTCTCCACTCTCGGGCGGGTCTG	960
Db	904	CTCTCGGCCACTACTCTTTTTTCCCTCTTCTCTGGGCTCTCCACTCTCTGGGCGGGTCTG	963

Qy	961	AGCCTACCTGAGCCCATGCAAGCTGGGGCCACATGCCAAAGTCAGGCCCTGGTTCCTTCTG	1020
Db	964	AGCCTACCTGAGCCCATGCAAGCTGGGGCCACATGCCAAAGTCAGGCCCTGGTTCCTTCTG	1023
Qy	1021	TCCTGTTTGGTAATAAACACATTCACGTTTCATGCTTCGAGGGCATTTTTCAAAAAAAA	1080
Db	1024	TCCTGTTTGGTAATAAACACATTCACGTTTCATGCTTCGAGGGCATTCCTTCAAAAAAAA	1083
Qy	1081	AAAAAAAAAAAAAAAAA 1097	
Db	1084	AAAAAAAAAAAAAAAAA 1100	
RESULT 9			
ABX96228			
ID	ABX96228	standard; cDNA; 1100 BP.	
XX	AC	ABX96228;	
XX	DT	13-MAY-2003 (first entry)	
XX	DE	Human secreted/transmembrane protein CDNA, #47.	
XX	XX	Human; Gene; ss; PRO; secreted; transmembrane; pharmaceutical;	
KW	KW	diagnostic; biosensor; biofactor; therapeutic; hyperplasia;	
KW	KW	endometriosis; cancer; tumour; ischaemia; coronary arterial disease;	
KW	KW	polycystic kidney disease; renal failure; inflammatory response; asthma;	
KW	KW	rheumatoid arthritis; psoriasis; multiple sclerosis; gene therapy;	
KW	KW	cytostatic; gynecological; cardiac; nephrotropic; hepatotropic;	
KW	KW	antiinflammatory.	
OS	XX	Homo sapiens.	
XX	XX	US2002160374-A1.	
PN	XX	31-OCT-2002.	
PD	XX	12-JUL-2001; 2001US-00905291.	
XX	PF	17-SEP-1997; 97US-0059113P.	
PR	PR	17-SEP-1997; 97US-0059115P.	
PR	PR	17-SEP-1997; 97US-0059117P.	
PR	PR	17-SEP-1997; 97US-0059119P.	
PR	PR	17-SEP-1997; 97US-0059121P.	
PR	PR	17-SEP-1997; 97US-0059122P.	
PR	PR	18-SEP-1997; 97US-0059184P.	
PR	PR	18-SEP-1997; 97US-0059263P.	
PR	PR	18-SEP-1997; 97US-0059266P.	
PR	PR	15-OCT-1997; 97US-0062125P.	
PR	PR	17-OCT-1997; 97US-0062285P.	
PR	PR	17-OCT-1997; 97US-0062287P.	
PR	PR	21-OCT-1997; 97US-0063486P.	
PR	PR	24-OCT-1997; 97US-0062814P.	
PR	PR	24-OCT-1997; 97US-0062816P.	
PR	PR	24-OCT-1997; 97US-0063045P.	
PR	PR	24-OCT-1997; 97US-0063120P.	
PR	PR	24-OCT-1997; 97US-0063121P.	
PR	PR	24-OCT-1997; 97US-0063127P.	
PR	PR	24-OCT-1997; 97US-0063128P.	
PR	PR	27-OCT-1997; 97US-0063327P.	
PR	PR	27-OCT-1997; 97US-0063329P.	
PR	PR	28-OCT-1997; 97US-0063541P.	
PR	PR	28-OCT-1997; 97US-0063542P.	
PR	PR	28-OCT-1997; 97US-0063544P.	
PR	PR	28-OCT-1997; 97US-0063549P.	
PR	PR	28-OCT-1997; 97US-0063550P.	
PR	PR	28-OCT-1997; 97US-0063564P.	
PR	PR	29-OCT-1997; 97US-0063435P.	
PR	PR	29-OCT-1997; 97US-0063704P.	
PR	PR	29-OCT-1997; 97US-0063732P.	
PR	PR	29-OCT-1997; 97US-0063734P.	
PR	PR	29-OCT-1997; 97US-0063735P.	


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PR 24-OCT-1997; 97US-0063121P.
PR 24-OCT-1997; 97US-0063127P.
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PR 27-OCT-1997; 97US-0063329P.
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PR 28-OCT-1997; 97US-0063542P.
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PR 28-OCT-1997; 97US-0063549P.
PR 28-OCT-1997; 97US-0063550P.
PR 28-OCT-1997; 97US-0063564P.
PR 28-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063732P.
PR 29-OCT-1997; 97US-0063734P.
PR 29-OCT-1997; 97US-0063735P.
PR 29-OCT-1997; 97US-0063738P.
PR 29-OCT-1997; 97US-0064215P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065185P.
PR 17-NOV-1997; 97US-0065848P.
PR 18-NOV-1997; 97US-0065693P.
PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0066772P.
PR 25-NOV-1997; 97US-0066840P.
PR 12-DEC-1997; 97US-0069425P.
PR 04-JUN-1998; 98US-0088026P.
PR 10-SEP-1998; 98US-0099803P.
PR 10-SEP-1998; 98WO-US018834P.
PR 14-SEP-1998; 98US-0100262P.
PR 14-SEP-1998; 98WO-US019177P.
PR 16-SEP-1998; 98WO-US019330P.
PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98WO-US019437P.
PR 13-OCT-1998; 98US-0104080P.
PR 20-NOV-1998; 98US-0109304P.
PR 01-DEC-1998; 98WO-US025108P.
PR 22-DEC-1998; 98US-0113296P.
PR 07-JUL-1999; 98US-0143048P.
PR 26-JUL-1999; 98US-0145698P.
PR 28-JUL-1999; 98WO-US020594P.
PR 08-SEP-1999; 99WO-US020594P.
PR 13-SEP-1999; 99WO-US020944P.
PR 15-SEP-1999; 99WO-US021090P.
PR 15-SEP-1999; 99WO-US021547P.
PR 05-OCT-1999; 99WO-US023089P.
PR 30-NOV-1999; 99WO-US028214P.
PR 30-NOV-1999; 99WO-US028313P.
PR 01-DEC-1999; 99WO-US028301P.
PR 02-DEC-1999; 99WO-US028564P.
PR 02-DEC-1999; 99WO-US028565P.
PR 16-DEC-1999; 99WO-US030095P.
PR 20-DEC-1999; 99WO-US030911P.
PR 20-DEC-1999; 99WO-US030999P.
PR 05-JAN-2000; 2000WO-US000219P.
PR 11-FEB-2000; 2000WO-US003565P.
PR 22-FEB-2000; 2000WO-US00414P.
PR 24-FEB-2000; 2000WO-US005004P.
PR 02-MAR-2000; 2000WO-US005841P.
PR 20-MAR-2000; 2000WO-US007377P.
PR 30-MAR-2000; 2000WO-US008439P.
PR 22-MAY-2000; 2000WO-US014042P.
PR 02-JUN-2000; 2000WO-US015264P.
PR 28-JUL-2000; 2000WO-US020710P.
PR 24-AUG-2000; 2000WO-US023328P.

PR 18-SEP-2000; 2000US-00665350.
(PGTH ) GENENTECH INC.
Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
Williams PM, Wood WI;
WPI; 2003-417923/39.
P-PSDB; ABO14909.
Novel secreted and transmembrane polypeptide for modulating biological
activity of cell expressing the polypeptide, identifying agonists or
antagonists of polypeptide, and as molecular weight markers.
Claim 2; Fig 91; 469pp; English.
The invention relates to an isolated, secreted and transmembrane
polypeptide, termed PRO polypeptide. The polypeptide is useful for
identifying agonists or antagonists of the polypeptide, for preparing
variants of the polypeptide, as molecular weight markers for protein
electrophoresis purposes and the nucleic acid is useful for recombinantly
expressing those markers. The polypeptide is also useful as therapeutic
agent. PRO is useful in assays to identify other proteins or molecules
involved in binding interaction. The nucleic acid is useful as
hybridisation probes, in chromosome and gene mapping, in generation of
antisense RNA and DNA, in the preparation of PRO polypeptide, for
generating transgenic animals or knockout animals which in turn are
useful in the development and screening of therapeutically useful
reagents, to construct hybridisation probes for mapping the gene which
encodes the PRO and for the genetic analysis of individuals with genetic
disorders, in gene therapy, for chromosome identification, as chromosome
marker, and for generating probes for polymerase chain reaction (PCR),
Northern analysis, Southern analysis and Western analysis. PRO antibody
is useful in diagnostic assays for PRO, e.g. detecting its expression in
specific cells, tissues or serum and for affinity purification of PRO
from recombinant cell culture or natural sources. The polypeptide or its
antibody is useful for the preparation of medicament for treating
conditions which is responsive to the PRO polypeptide or anti-PRO
antibody e.g. tumour. The polypeptide and the nucleic acid is useful for
tissue typing. The polypeptide is useful for treating obesity, diabetes
or hypo- or hyper-insulinaemia and cardiac insufficiency disorders, for
inhibiting tumour growth, enhances vascular permeability and immune
response, for inducing regeneration of auditory hair cells and for
treating hearing loss in mammals and for treating bone and/or cartilage
disorders such as sports injuries and arthritis. The present sequence
represents cDNA encoding a human secreted and transmembrane PRO
polypeptide
SQ Sequence 1100 BP; 225 A; 321 C; 314 G; 240 T; 0 U; 0 Other;
Query Match 99.1%; Score 1090.6; DB 8; Length 1100;
Best Local Similarity 99.6%; Pred. No. 4.4e-227;
Matches 1093; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 CGCGGGAGAGGAGCCATGGCGCGCGCGGGGGCGCTGCTGGCGCTGCTGCTGCTG 60
Db 4 CGCGGGAGAGGAGCCATGGCGCGCGCGGGGGCGCTGCTGGCGCTGCTGCTGCTG 63
QY 61 GGCTGGACTCAGGAAGCCGGAGTCCGAGAGGCGCGCGCGCTTATCAGGACCATCGCGCCG 120
Db 64 GGCTGGACTCAGGAAGCCGGAGTCCGAGAGGCGCGCGCTTATCAGGACCATCGCGCCG 123
QY 121 ACGGGTCATCATCGTCGCGCATCGTGGTGGAGAGACGCCGAACTCGGGCGTTGGCGGT 180
Db 124 ACGGGTCATCATCGTCGCGCATCGTGGTGGAGAGACGCCGAACTCGGGCGTTGGCGGT 183
QY 181 GCAGGGGAGCGCTCGCGCTGTGGATTCCACCGTATCGGAGTGAGCTGCTAGCCACCG 240
Db 184 GCAGGGGAGCGCTCGCGCTGTGGATTCCACCGTATCGGAGTGAGCTGCTAGCCACCG 243
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Db 1024 TCTGTTGGTAATAACACATCCAGTTGATGCTTCAGGGCAATTTCTCAAAAAAAAA 1083
QY 1081 AAAAAAAAAAAAAA 1097
Db 1084 AAAAAAAAAAAAAA 1100
RESULT 13
ACD19854
ID ACD19854 standard; cDNA; 1100 BP.
XX AC ACD19854;
XX 22-AUG-2003 (first entry)
XX Human secreted / transmembrane polypeptide PRO303 cDNA.
KW Human; ss; gene; gene therapy; apoptosis; bleeding; tumour; ALS;
KW gynaecological disease; hysterectomy; angiogenesis; skin disease; cancer;
KW coronary ischaemic condition; gastrointestinal mucosa disorder; asthma;
KW mucosal lesion repair; keratinocyte differentiation; psoriasis;
KW Parkinson's disease; Alzheimer's disease; amyotrophic lateral sclerosis;
KW neuropathy; blood coagulation cascade disorder; thrombosis; haemorrhage;
KW neurodegenerative disease; endometrial bleeding; wound healing; tissue repair; rheumatoid arthritis; multiple sclerosis; tissue typing.
XX OS Homo sapiens.
XX FN US2003027143-A1.
XX PD 06-FEB-2003.
XX 16-JUL-2001; 2001US-00906838.
PR 17-SEP-1997; 97US-0059113P.
PR 17-SEP-1997; 97US-0059115P.
PR 17-SEP-1997; 97US-0059117P.
PR 17-SEP-1997; 97US-0059119P.
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PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 15-OCT-1997; 97US-0062125P.
PR 17-OCT-1997; 97US-0062285P.
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PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0062814P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063045P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 24-OCT-1997; 97US-0063127P.
PR 24-OCT-1997; 97US-0063128P.
PR 27-OCT-1997; 97US-0063327P.
PR 27-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-0063341P.
PR 28-OCT-1997; 97US-0063342P.
PR 28-OCT-1997; 97US-0063344P.
PR 28-OCT-1997; 97US-0063349P.
PR 28-OCT-1997; 97US-0063550P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063732P.
PR 29-OCT-1997; 97US-0063734P.
PR 29-OCT-1997; 97US-0063735P.
PR 29-OCT-1997; 97US-0063738P.
PR 31-OCT-1997; 97US-0064215P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 18-NOV-1997; 97US-0065693P.
PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0066772P.
PR 25-NOV-1997; 97US-0066840P.
PR 12-DEC-1997; 97US-0069425P.
PR 04-JUN-1998; 98US-0088026P.
PR 10-SEP-1998; 98US-0099803P.
PR 14-SEP-1998; 98US-0100262P.
PR 14-SEP-1998; 98US-0100262P.
PR 16-SEP-1998; 98US-0100262P.
PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98US-0100858P.
PR 13-OCT-1998; 98US-0104080P.
PR 20-NOV-1998; 98US-0109304P.
PR 01-DEC-1998; 98US-0109304P.
PR 22-DEC-1998; 98US-0113296P.
PR 07-JUL-1999; 99US-0143048P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 08-SEP-1999; 99US-0146222P.
PR 13-SEP-1999; 99US-0146222P.
PR 15-SEP-1999; 99US-0146222P.
PR 15-SEP-1999; 99US-0146222P.
PR 05-OCT-1999; 99US-0146222P.
PR 29-NOV-1999; 99US-0146222P.
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PR 02-DEC-1999; 99US-0146222P.
PR 16-DEC-1999; 99US-0146222P.
PR 20-DEC-1999; 99US-0146222P.
PR 20-DEC-1999; 99US-0146222P.
PR 05-JAN-2000; 2000US-0000219.
PR 11-FEB-2000; 2000US-0000356.
PR 22-FEB-2000; 2000US-0000414.
PR 24-FEB-2000; 2000US-0000504.
PR 02-MAR-2000; 2000US-0000581.
PR 30-MAR-2000; 2000US-0000737.
PR 30-MAR-2000; 2000US-0000843.
PR 22-MAY-2000; 2000US-0014042.
PR 02-JUN-2000; 2000US-0015264.
PR 28-JUL-2000; 2000US-0020710.
PR 24-AUG-2000; 2000US-0023328.
PR 18-SEP-2000; 2000US-00665350.
(GETH) GENENTECH INC.
XX Ashkenazi A, Botstein D, Desnovers L, Eaton DL, Ferrara N;
XX Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
XX Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
XX Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
XX Williams PM, Wood WI;
XX WPI; 2003-417249/39.
XX P-PSDB; ABO14848.
XX Novel secreted and transmembrane polypeptides and polynucleotides
XX encoding them useful for treating abnormal bleeding involved in
XX gynecological diseases, skin diseases and neurodegenerative diseases.
XX Claim 2; Fig 91; 467pp; English.
XX The invention relates to an isolated secreted and transmembrane PRO
XX polypeptide. The PRO polypeptides are useful for modulating biological
XX activity of a cell, in diagnosing or treating abnormal bleeding involved

PR 24-OCT-1997; 97US-0062816P.
 PR 24-OCT-1997; 97US-0063045P.
 PR 24-OCT-1997; 97US-0063120P.
 PR 24-OCT-1997; 97US-0063121P.
 PR 24-OCT-1997; 97US-0063127P.
 PR 24-OCT-1997; 97US-0063128P.
 PR 27-OCT-1997; 97US-0063327P.
 PR 27-OCT-1997; 97US-0063329P.
 PR 28-OCT-1997; 97US-0063541P.
 PR 28-OCT-1997; 97US-0063542P.
 PR 28-OCT-1997; 97US-0063544P.
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 PR 29-OCT-1997; 97US-0063732P.
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 PR 29-OCT-1997; 97US-0063738P.
 PR 29-OCT-1997; 97US-0064215P.
 PR 31-OCT-1997; 97US-0064103P.
 PR 01-NOV-1997; 97US-0064248P.
 PR 07-NOV-1997; 97US-0064809P.
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 PR 17-NOV-1997; 97US-0065846P.
 PR 18-NOV-1997; 97US-0065693P.
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 PR 04-JUN-1998; 98US-0088026P.
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 PR 10-SEP-1998; 98WO-US018824.
 PR 14-SEP-1998; 98US-0100262P.
 PR 14-SEP-1998; 98WO-US019177.
 PR 16-SEP-1998; 98WO-US019330.
 PR 17-SEP-1998; 98US-0100858P.
 PR 17-SEP-1998; 98WO-US019437.
 PR 13-OCT-1998; 98US-0104080P.
 PR 20-NOV-1998; 98US-0109304P.
 PR 01-DEC-1998; 98WO-US025108.
 PR 22-DEC-1998; 98US-0113296P.
 PR 07-JUL-1999; 99US-0143048P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 28-JUL-1999; 99US-0146222P.
 PR 08-SEP-1999; 99WO-US020594.
 PR 13-SEP-1999; 99WO-US020944.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 05-OCT-1999; 99WO-US023089.
 PR 29-NOV-1999; 99WO-US028214.
 PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028301.
 PR 02-DEC-1999; 99WO-US028564.
 PR 02-DEC-1999; 99WO-US028565.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 20-DEC-1999; 99WO-US030999.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US005044.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 22-MAY-2000; 2000WO-US014042.

PR 02-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 18-SEP-2000; 2000US-00665350.
 XX (GETH) GENENTECH INC.
 PA
 XX Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ, Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D, Williams PM, Wood WI;
 XX WPI; 2003-765473/72.
 DR P-PSDB; ADB29462.
 DR
 XX
 PT Novel isolated native PRO polypeptide useful for treating Parkinson's disease, enterocolitis, Zollinger-Ellison syndrome gastrointestinal ulceration, Alzheimer's disease, amyotrophic lateral sclerosis, Usher syndrome.
 PT
 XX
 PS Claim 2; Fig 91; 469pp; English.
 XX
 CC The invention discloses isolated PRO secreted/transmembrane polypeptides and the nucleic acid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide, for linking a bioactive molecule to a cell expressing a PRO protein and for modulating at least one biological activity of a cell. PRO polypeptides are useful for detecting other PRO polypeptides in a sample and for linking a bioactive molecule to a cell expressing a PRO polypeptide. The PRO polypeptide antibodies are useful for modulating the biological activity of a cell expressing PRO polypeptides. PRO polypeptides are also useful for treating disorders associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal lesions, skin diseases associated with abnormal keratinocyte differentiation (e.g. psoriasis), Parkinson's disease, Alzheimer's disease, amyotrophic lateral sclerosis (ALS), neuropathies and additionally, disease related to uncontrolled cell growth, e.g. cancer. PRO polypeptides also serves as tumour specific antigens which may be exploited as therapeutic targets for anti-tumour drugs, and are also employed therapeutically in vivo for lessening the effects of viral infection. The PRO polypeptides can be also used in assays to determine if it has a role in neurodegenerative diseases or their reversal, as an antithrombotic agent with reduced risk for haemorrhage as compared with heparin, in treating other PRO-associated disorders, in modulating endometrial bleeding angiogenesis, and may also have an effect on kidney tissue. PRO polypeptides and their portions affect the expression of genes which have a role in apoptosis. The polynucleotides are useful in molecular biology including uses as hybridisation probes for cDNA library to isolate the full-length PRO cDNA or to isolate other cDNAs, in chromosome and gene mapping, in the generation of antisense RNA and DNA, for preparing PRO polypeptides, for generating transgenic animals or knockout animals which are useful in the development and screening of therapeutically useful reagents, as probes and for the genetic analysis of individuals with genetic disorders as well as for recombinantly expressing the protein and for chromosome identification. The proteins are useful as molecular marker for protein electrophoresis purposes, as therapeutic agents, for screening compounds to identify those that mimic the PRO polypeptide (agonists) or prevent the effect of the PRO polypeptide (antagonists). The polynucleotides and proteins are useful for tissue typing. PRO antibodies are useful for immunohistochemical staining and/or assay of sample fluids. Anti-PRO antibodies are useful in diagnostic assays for PRO e.g. detecting its expression in specific cells, tissues or serum and for affinity purification of PRO from recombinant cell culture or natural sources. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. The sequence presented is a gene encoding a PRO polynucleotide of the

XX
 SQ Sequence 1100 BP; 225 A; 321 C; 314 G; 240 T; 0 U; 0 Other;
 Query Match 99.1%; Score 1090.6; DB 9; Length 1100;
 Best Local Similarity 99.6%; Pred. No. 4.4e-227;

Matches 1093; Conservative 0; Mismatches 4; Indels 0; Gaps 0;			
QY	1	CGCGGAGAGAGGCGATGGCGCGCGCGCGCGCTGCTGCTGGCGCTGCTGCTGGCTCG	60
Db	4	CGCGGAGAGAGGCGATGGCGCGCGCGCGCGCTGCTGCTGGCGCTGCTGCTGGCTCG	63
QY	61	GGCTGCACTCAGGAAGCGGAGTGCAGAGGCGCGCGCTTATCAGGACCATCGGCGG	120
Db	64	GGCTGCACTCAGGAAGCGGAGTGCAGAGGCGCGCGCTTATCAGGACCATCGGCGG	123
QY	121	ACGGGTATCATCGTCGCGCATCGTGGGTGGAGAGAGCGCCCAACTCGGGCGTTGGCGGTG	180
Db	124	ACGGGTATCATCGTCGCGCATCGTGGGTGGAGAGAGCGCCCAACTCGGGCGTTGGCGGTG	183
QY	181	GCAGGGGAGCGCTGCGCTGCTGGGATTCACAGTATGCGGAGTGAGCTGCTCAGCCACCG	240
Db	184	GCAGGGGAGCGCTGCGCTGCTGGGATTCACAGTATGCGGAGTGAGCTGCTCAGCCACCG	243
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QY	301	GTGGATGCTCAGTTGCGGAGCTGACTTCCATGCGATCTCTCGAGCCTCGAGGCTA	360
Db	304	GTGGATGCTCAGTTGCGGAGCTGACTTCCATGCGATCTCTCGAGCCTCGAGGCTA	363
QY	361	CTACACCCGTTACTTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGGAATTCACC	420
Db	364	CTACACCCGTTACTTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGGAATTCACC	423
QY	421	CTATGACATTCGCTTGTGGAAGTGTCTGCACTGTCACTTACCTAACACACATCCAGCC	480
Db	424	CTATGACATTCGCTTGTGGAAGTGTCTGCACTGTCACTTACCTAACACACATCCAGCC	483
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QY	661	GGACATCTTTGGAGACATGTTGCTGGCAATGCCCAAGCGCGGAGAGTGCCTCTT	720
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QY	721	CGGTGACTCAGGTGGACCTTTGGCTGTAAACAAGGATGGACTGTGGTATCAGATTGGAGT	780
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QY	781	CGTGAGCTGGGAGTGGGCTGTGTGGCCCAATCGGCCCGGTGTCTACACCAATATCAG	840
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QY	901	CTCCTGGCCGCTACTCTTTTTCCTCTTCTGCGGCTCTCCACTCTCTGGGCGCGGTCTG	960
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QY	961	AGCCTACTGAGCCCATGACGCTGGGGCCCATCTGCCAAGTCAGGCCCTGGTTCTTCTG	1020
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QY	1021	TCCTGTTTGGTAATAACACATTCAGTTGATGCTTGCAGGGCATTTTTCAAAAAAA	1080
Db	1024	TCCTGTTTGGTAATAACACATTCAGTTGATGCTTGCAGGGCATTTTTCAAAAAAA	1083

QY	1081	AAAAAAAAAAAAAAAAAAAA 1097
Db	1084	AAAAAAAAAAAAAAAAAAAA 1100
RESULT 15		
ID	ADA18317	
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AC	ADA18317;	
XX	20-NOV-2003	(first entry)
XX	Human secreted/transmembrane protein cDNA, #49.	
XX	Human; gene; ss; PRO; secreted; transmembrane; gastrointestinal mucosa;	
KW	mucosal lesion; skin disease; keratinocyte differentiation; psoriasis;	
KW	Parkinson's disease; Alzheimer's diseases; amyotrophic lateral sclerosis;	
KW	ALS; neuropathy; cell growth; cancer; tumour; viral infection;	
KW	neurodegenerative disease; antithrombotic agent; haemorrhage;	
KW	endometrial bleeding angiogenesis; kidney tissue; apoptosis; therapeutic;	
KW	tissue typing; immunohistochemical staining; gene therapy; neurotropic;	
KW	neuroprotective; cytostatic; virucide; anticoagulant.	
OS	Homo sapiens.	
XX	US2003039971-A1.	
XX	27-FEB-2003.	
XX	16-JUL-2001; 2001US-00906646.	
XX	17-SEP-1997; 97US-0059113P.	
XX	17-SEP-1997; 97US-0059115P.	
XX	17-SEP-1997; 97US-0059117P.	
XX	17-SEP-1997; 97US-0059119P.	
XX	17-SEP-1997; 97US-0059121P.	
XX	17-SEP-1997; 97US-0059122P.	
XX	17-SEP-1997; 97US-0059184P.	
XX	18-SEP-1997; 97US-0059263P.	
XX	18-SEP-1997; 97US-0059266P.	
XX	15-OCT-1997; 97US-0062125P.	
XX	17-OCT-1997; 97US-0062285P.	
XX	17-OCT-1997; 97US-0062287P.	
XX	21-OCT-1997; 97US-0063486P.	
XX	24-OCT-1997; 97US-0062814P.	
XX	24-OCT-1997; 97US-0062816P.	
XX	24-OCT-1997; 97US-0063045P.	
XX	24-OCT-1997; 97US-0063120P.	
XX	24-OCT-1997; 97US-0063121P.	
XX	24-OCT-1997; 97US-0063127P.	
XX	24-OCT-1997; 97US-0063128P.	
XX	27-OCT-1997; 97US-0063327P.	
XX	27-OCT-1997; 97US-0063329P.	
XX	28-OCT-1997; 97US-0063541P.	
XX	28-OCT-1997; 97US-0063542P.	
XX	28-OCT-1997; 97US-0063544P.	
XX	28-OCT-1997; 97US-0063549P.	
XX	28-OCT-1997; 97US-0063550P.	
XX	28-OCT-1997; 97US-0063564P.	
XX	29-OCT-1997; 97US-0063435P.	
XX	29-OCT-1997; 97US-0063704P.	
XX	29-OCT-1997; 97US-0063732P.	
XX	29-OCT-1997; 97US-0063734P.	
XX	29-OCT-1997; 97US-0063735P.	
XX	29-OCT-1997; 97US-0063738P.	
XX	29-OCT-1997; 97US-0064215P.	
XX	31-OCT-1997; 97US-0063870P.	
XX	31-OCT-1997; 97US-0064103P.	
XX	03-NOV-1997; 97US-0064248P.	
XX	07-NOV-1997; 97US-0064809P.	
XX	12-NOV-1997; 97US-0065186P.	


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Db 424 |||||CTATGACATTCCTTGGTGAAGCTGTCTGCACTGTCTACCTTACACTAAACACATCCAGCC 483
QY 481 |||||CATCTGTCTCCAGGCTCCACATTTGAGTTTGAACCGGACAGACTGCTGGGTGACTGG 540
Db 484 |||||CATCTGTCTCCAGGCTCCACATTTGAGTTTGAACCGGACAGACTGCTGGGTGACTGG 543
QY 541 |||||CTGGGGTACATCAAGAGGATGAGGCACTGCGATCTCCCACTCCAGGAAGTTCA 600
Db 544 |||||CTGGGGTACATCAAGAGGATGAGGCACTGCGATCTCCCACTCCAGGAAGTTCA 603
QY 601 |||||GGTGGCCATATAAACAACCTCTATGTGCAACACCTCTTCTCAAGTACAGTTTCCGCAA 660
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